

FIG. 1

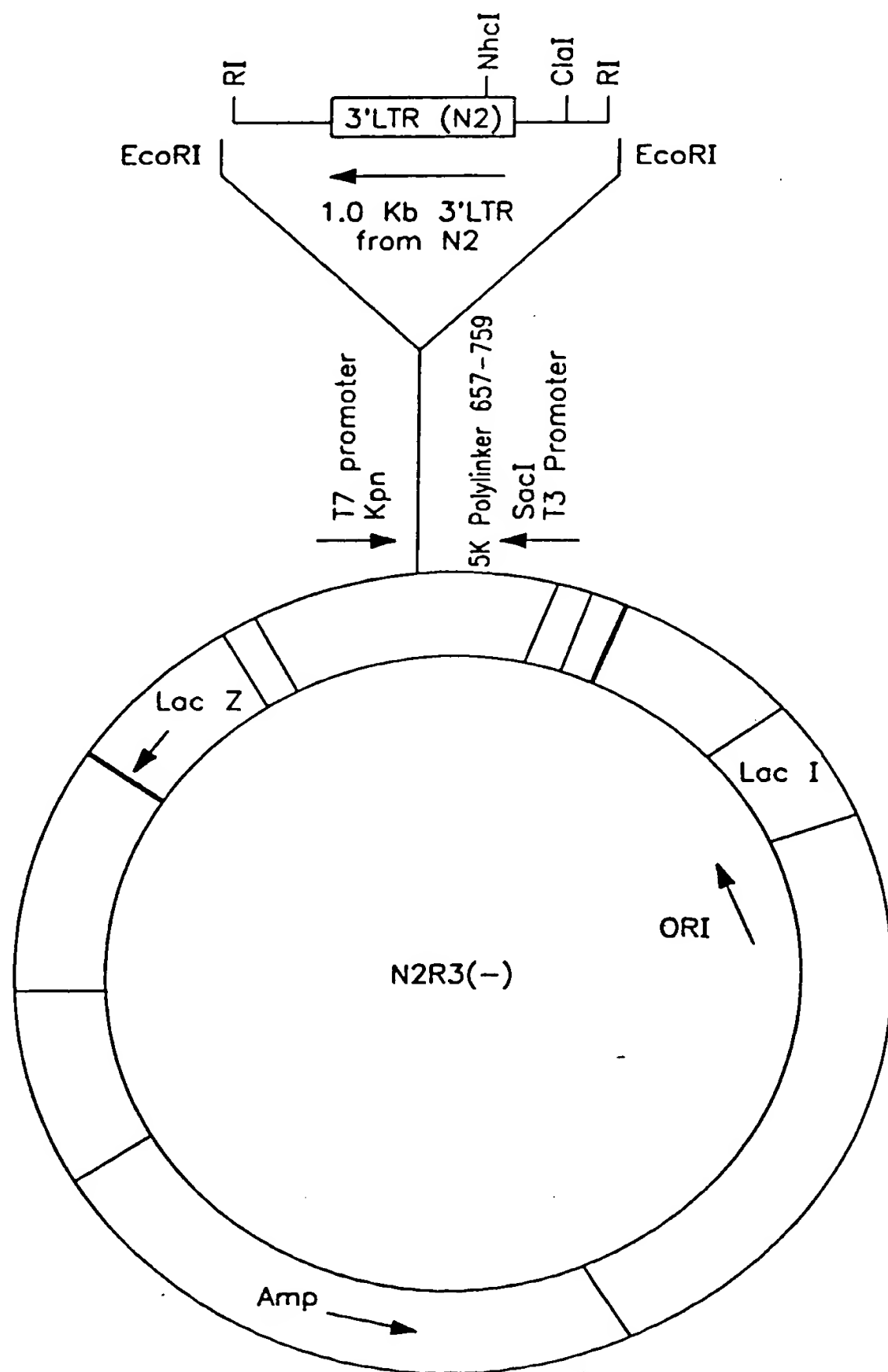


FIG. 2

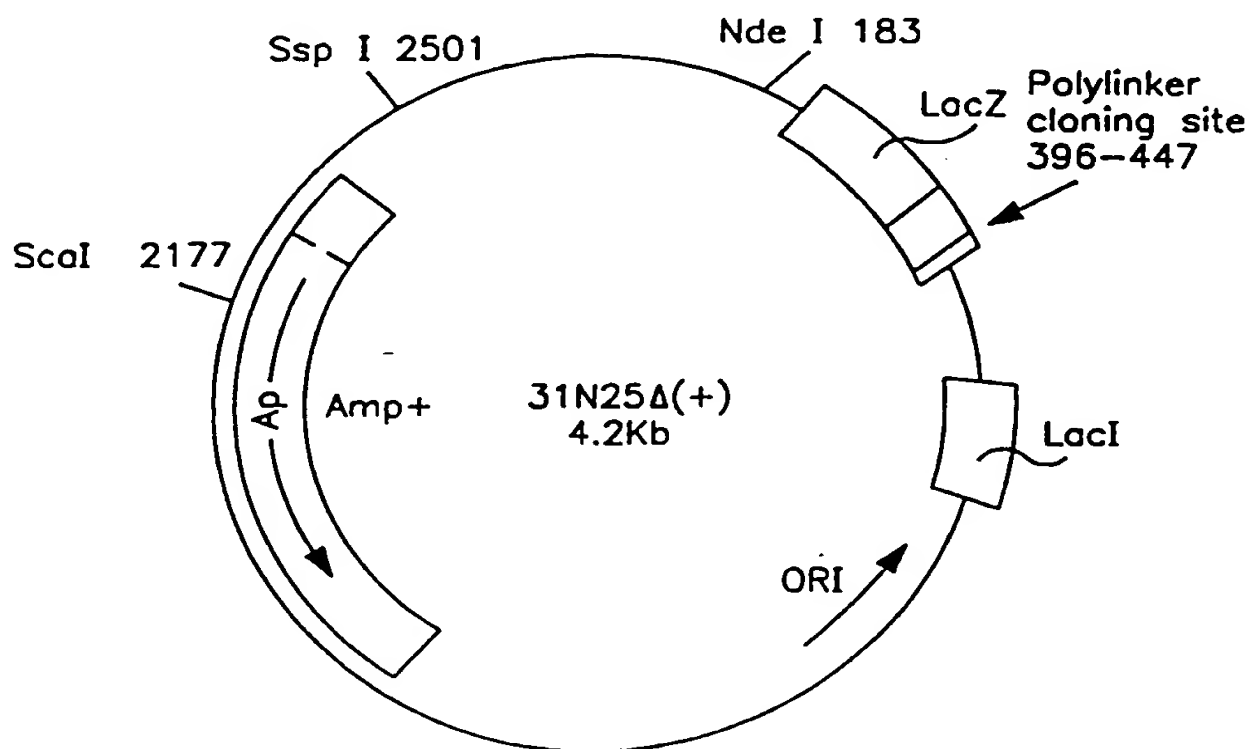
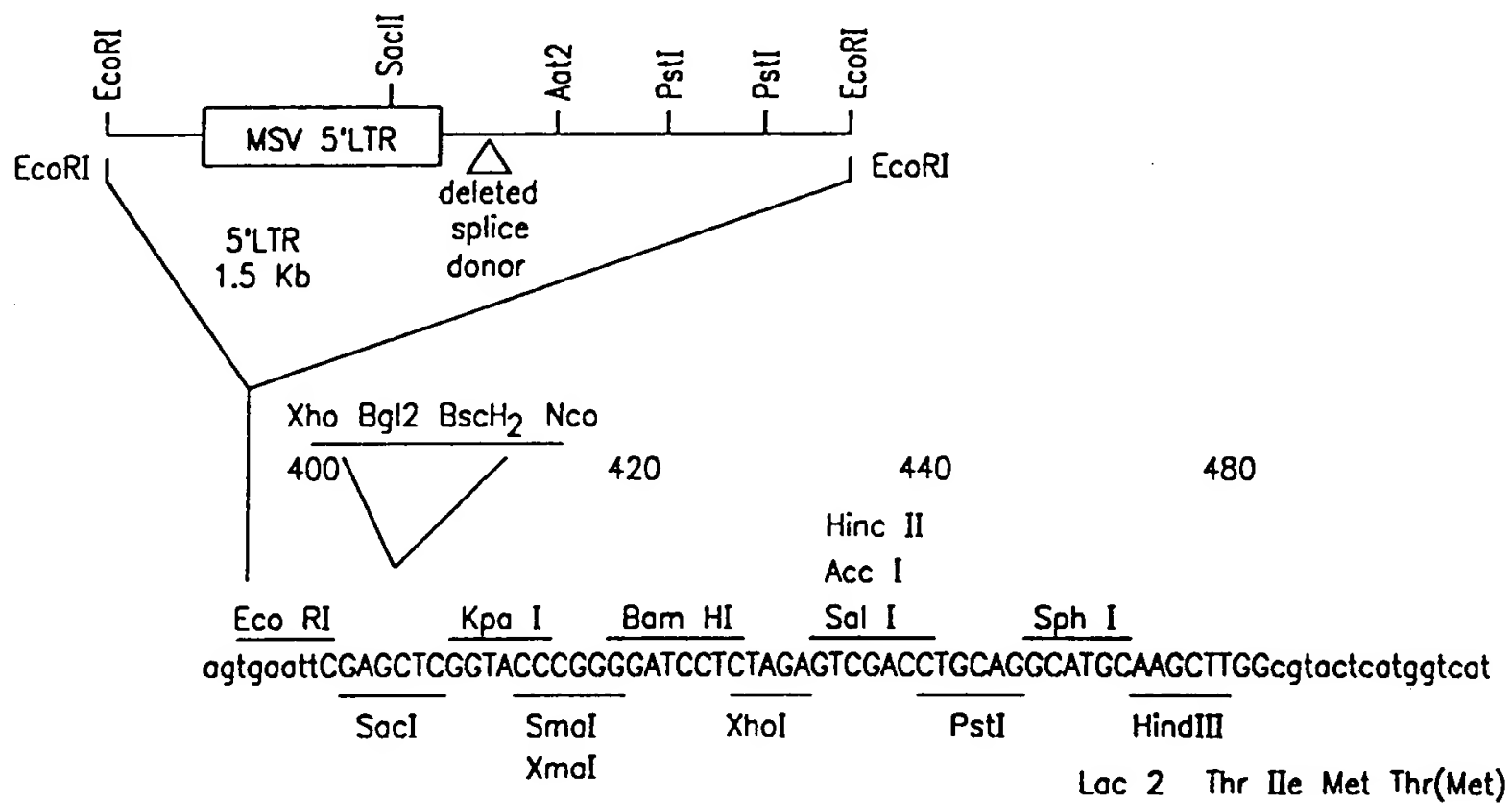


FIG. 3

17

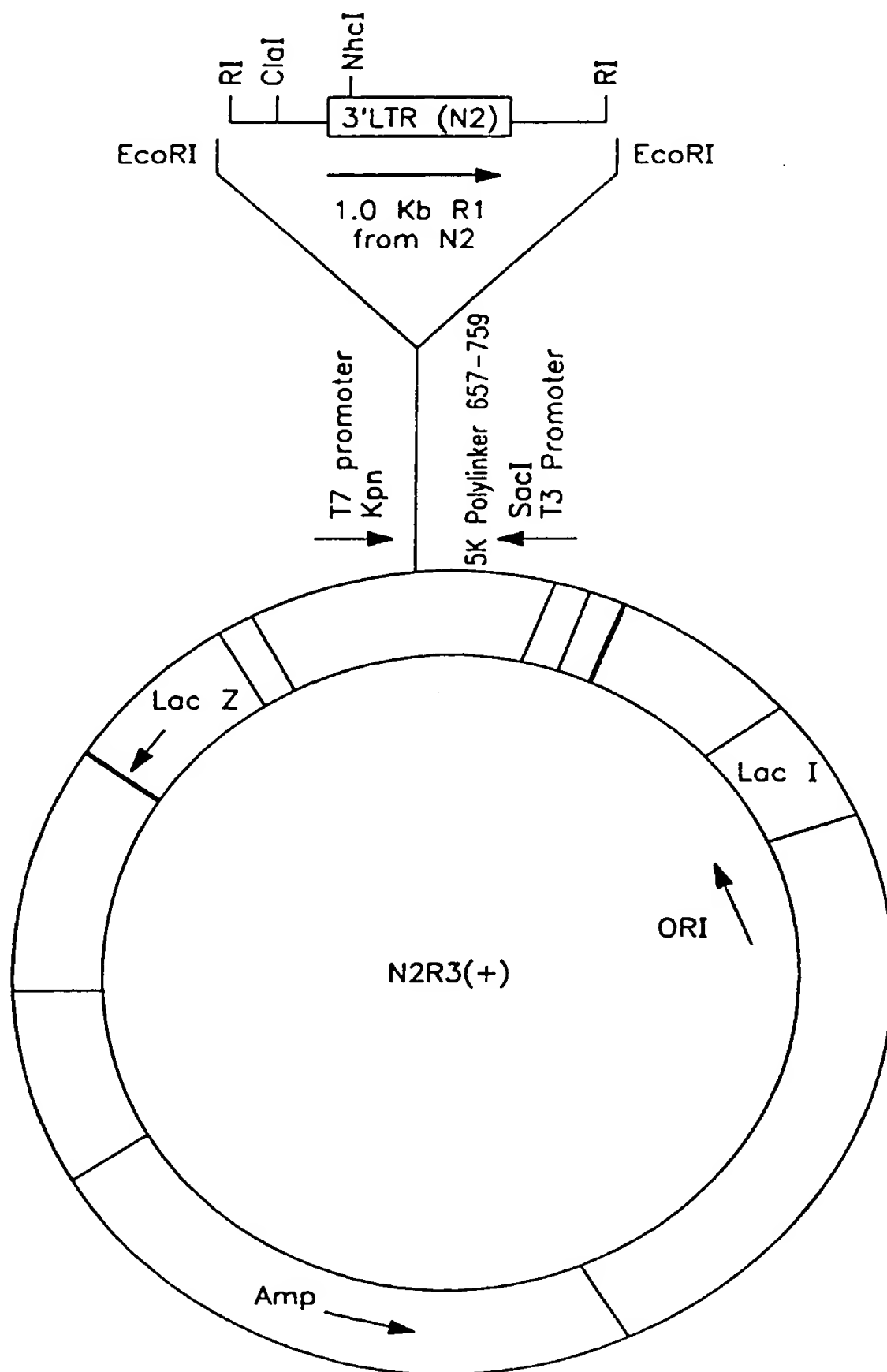


FIG. 4

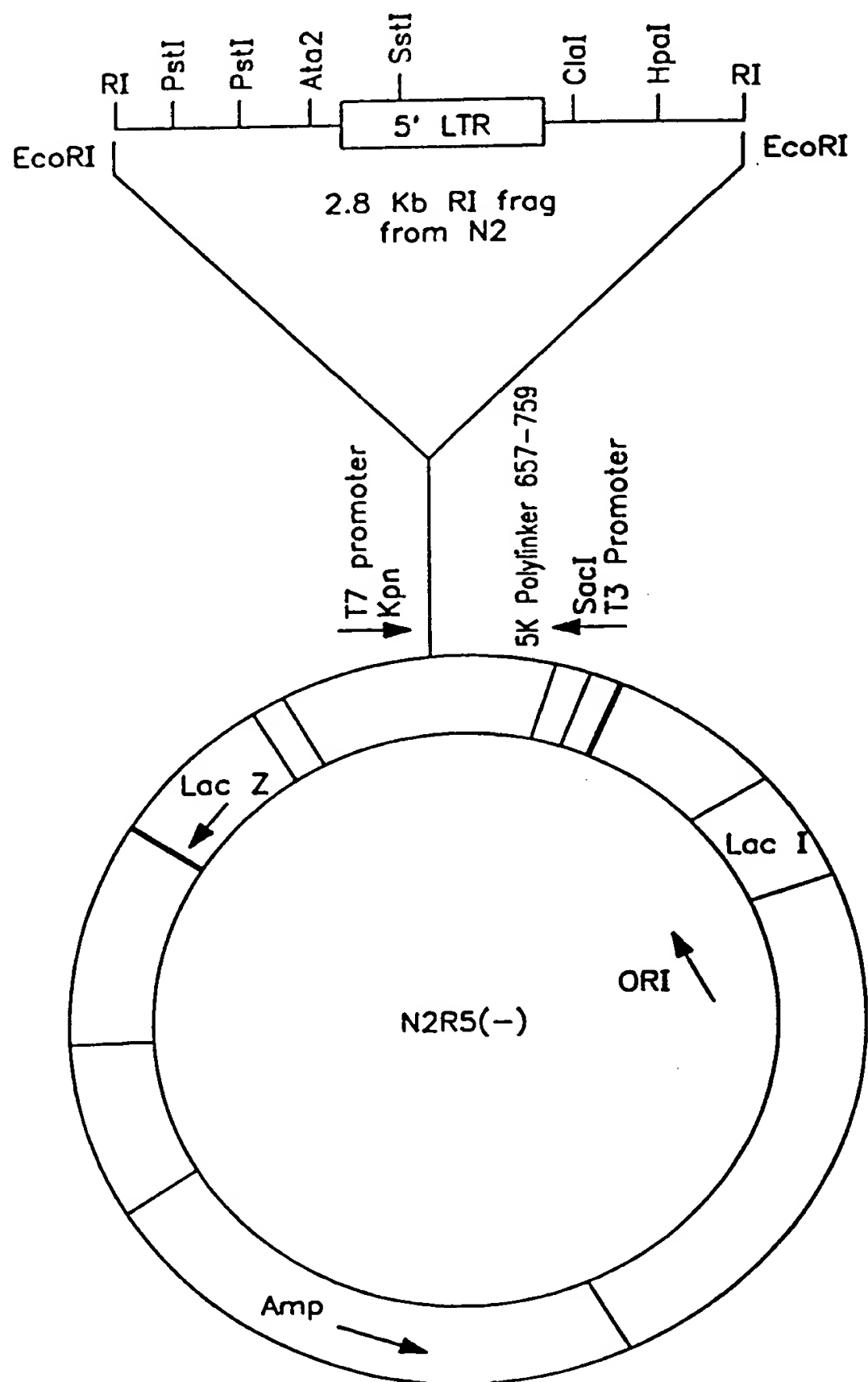


FIG. 5

4145

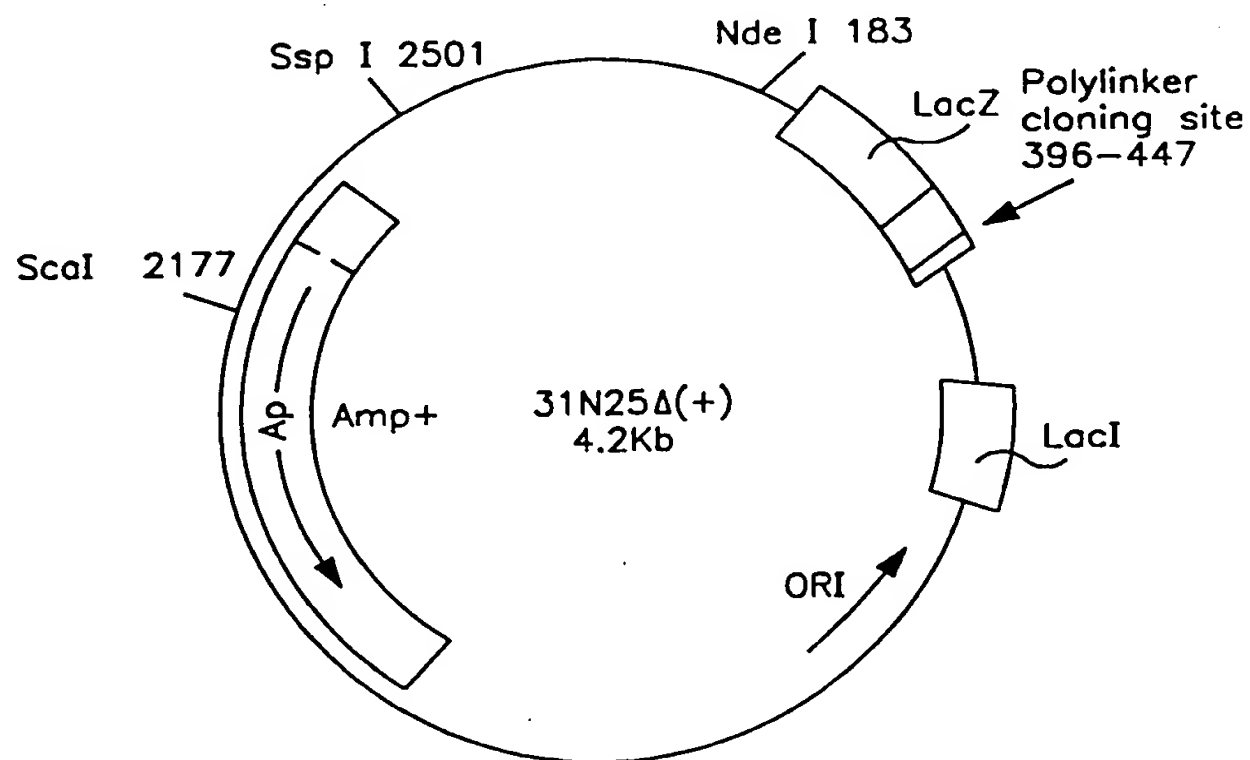
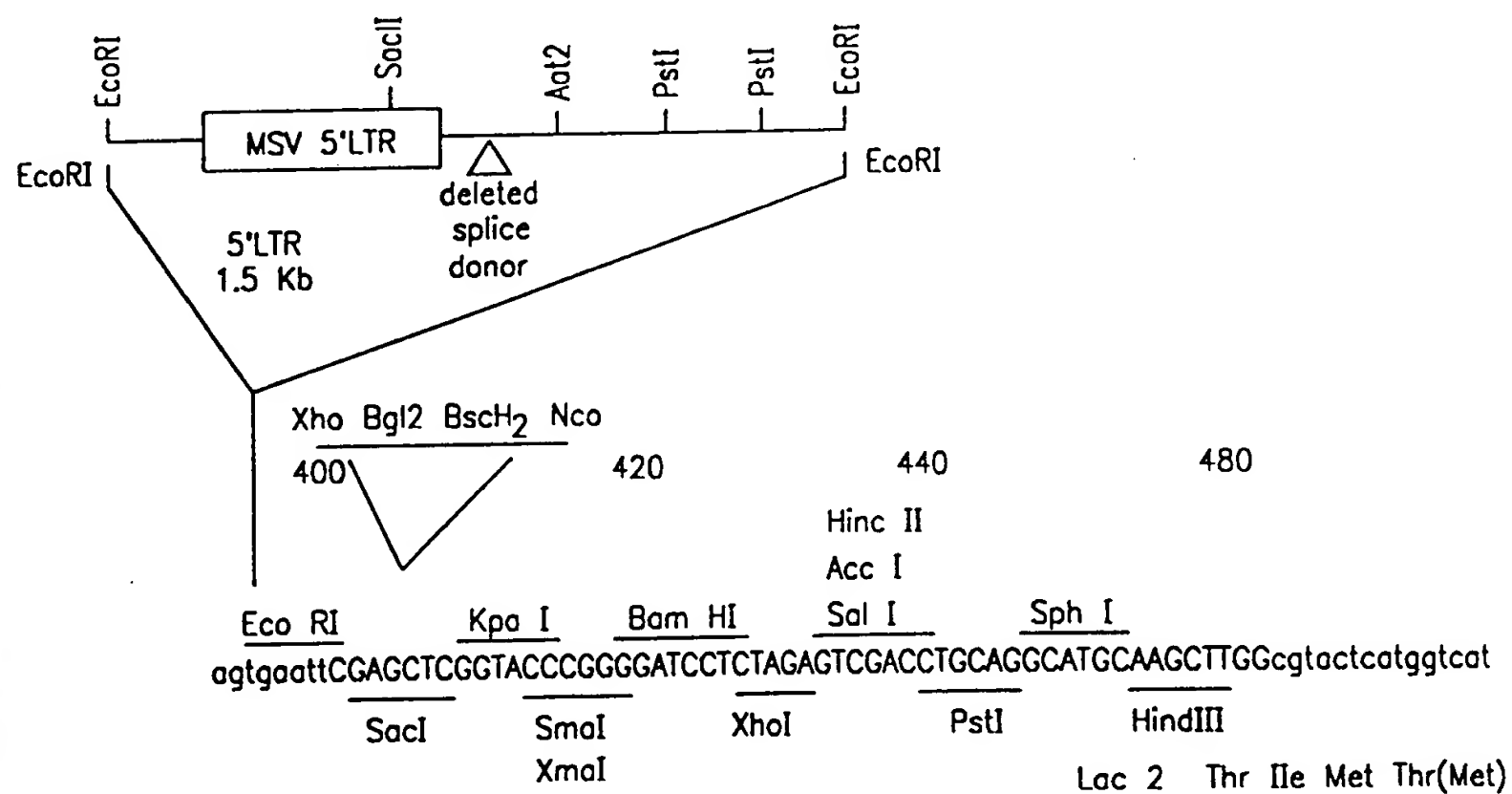


FIG. 6

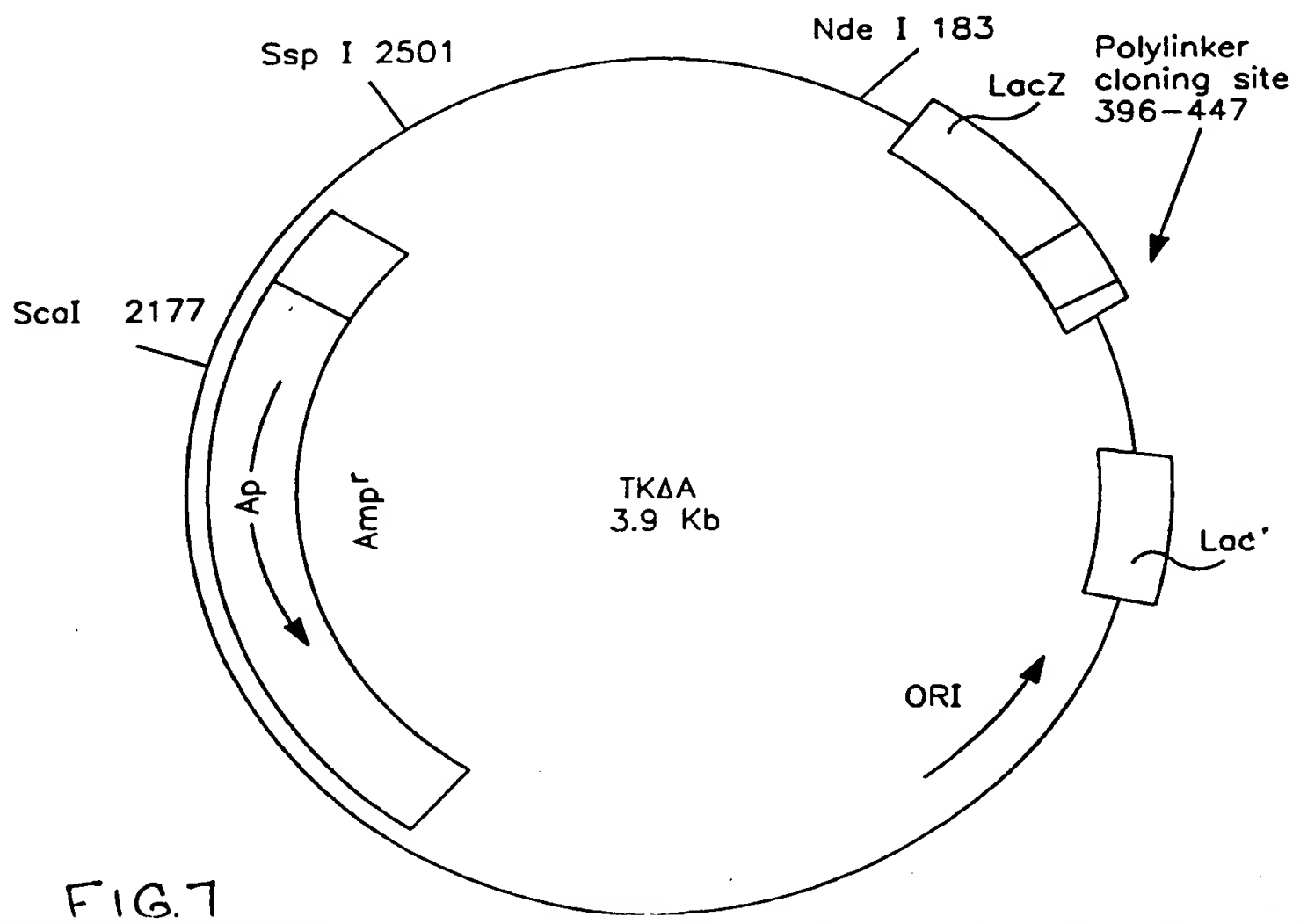
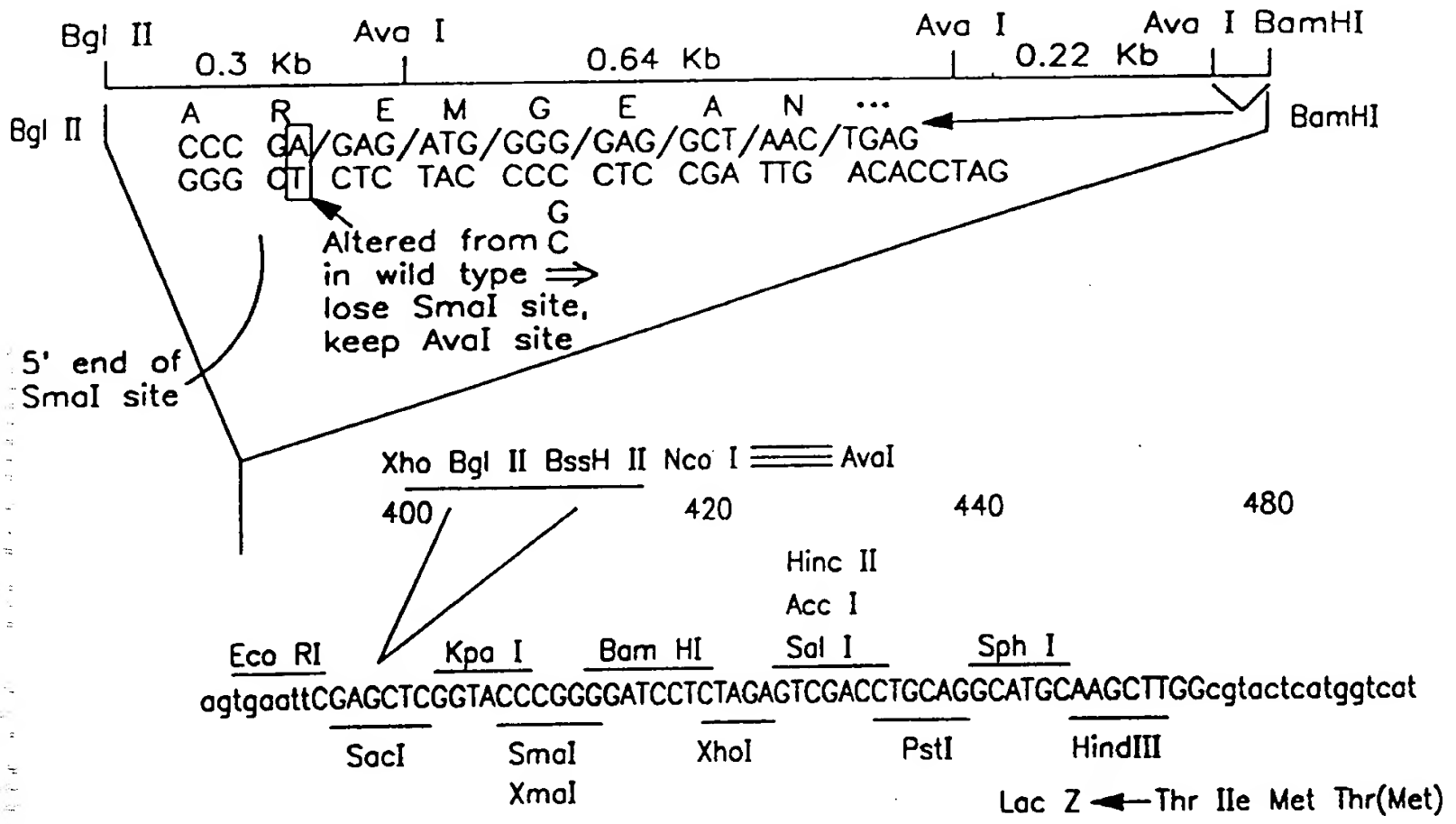


FIG. 7

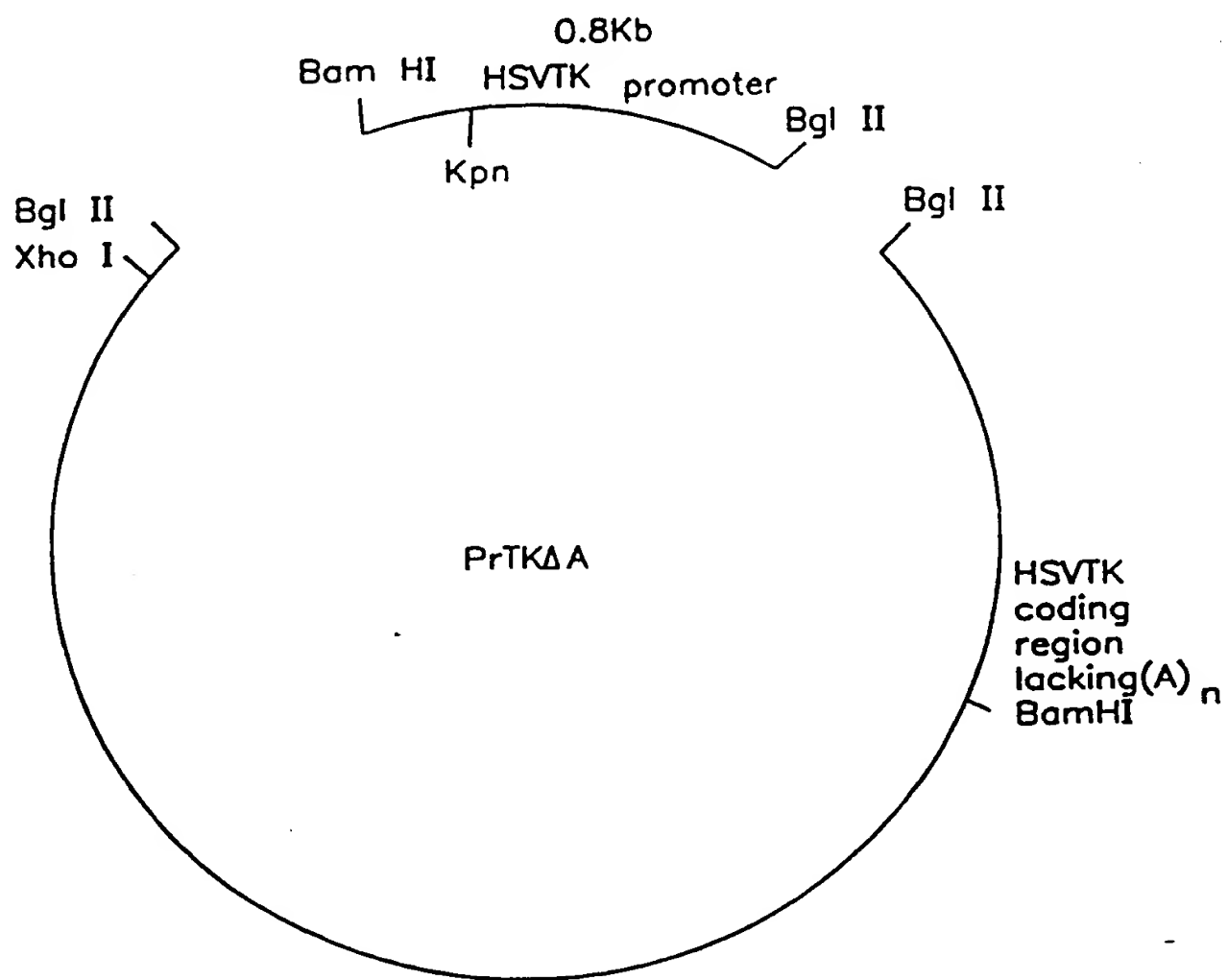


FIG. 8

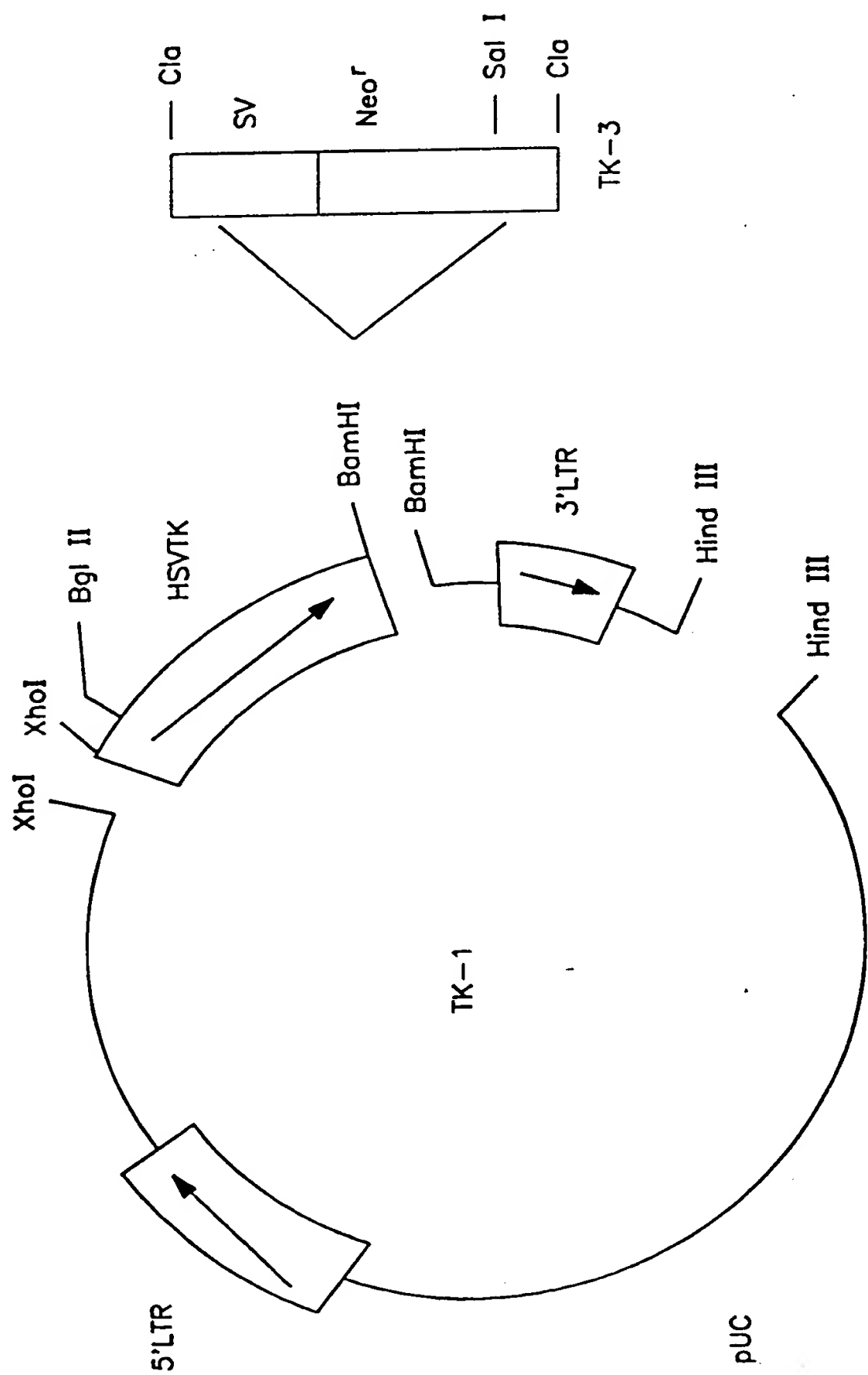


FIG. 9

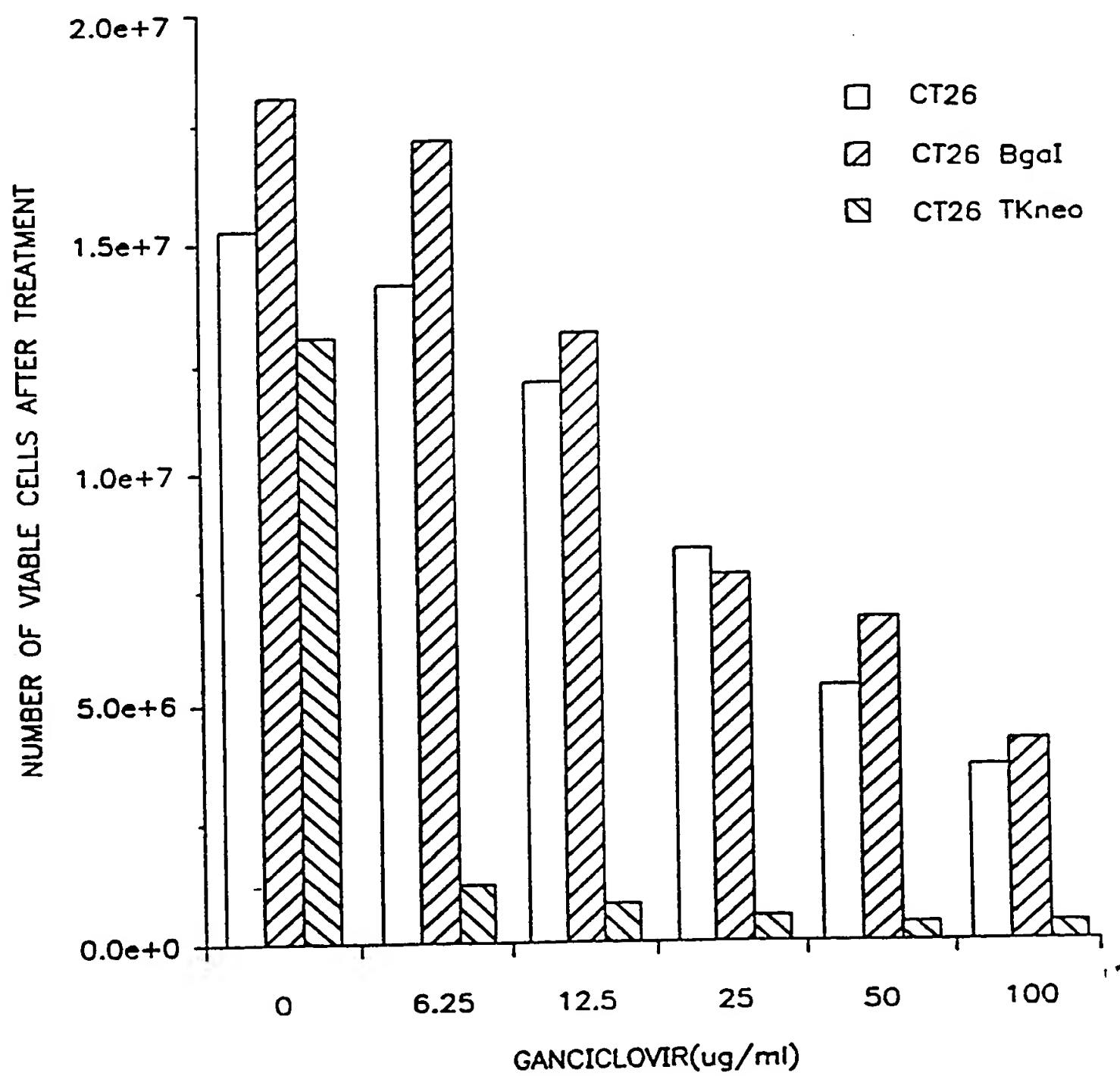


FIG. 10

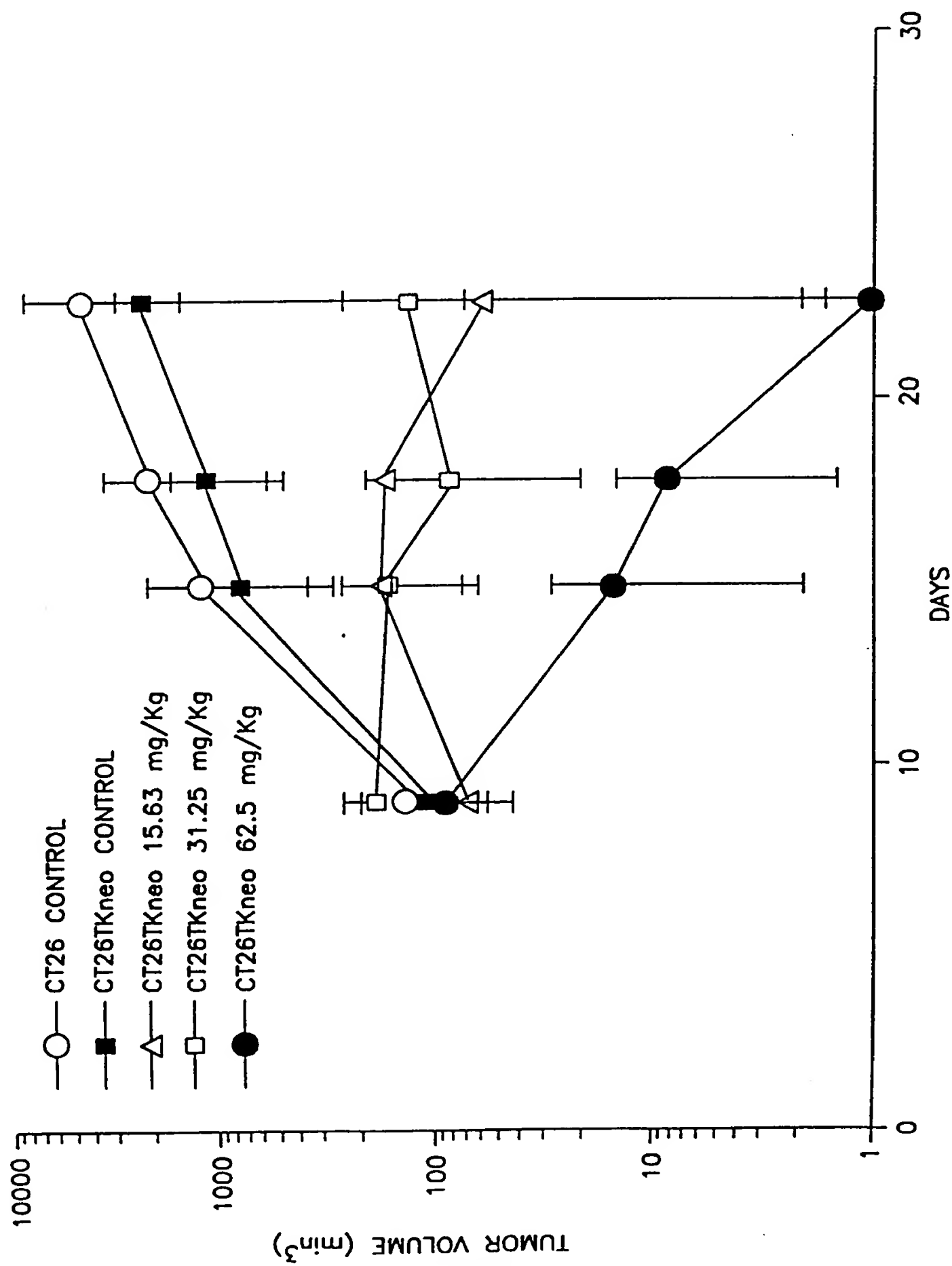


FIG. II

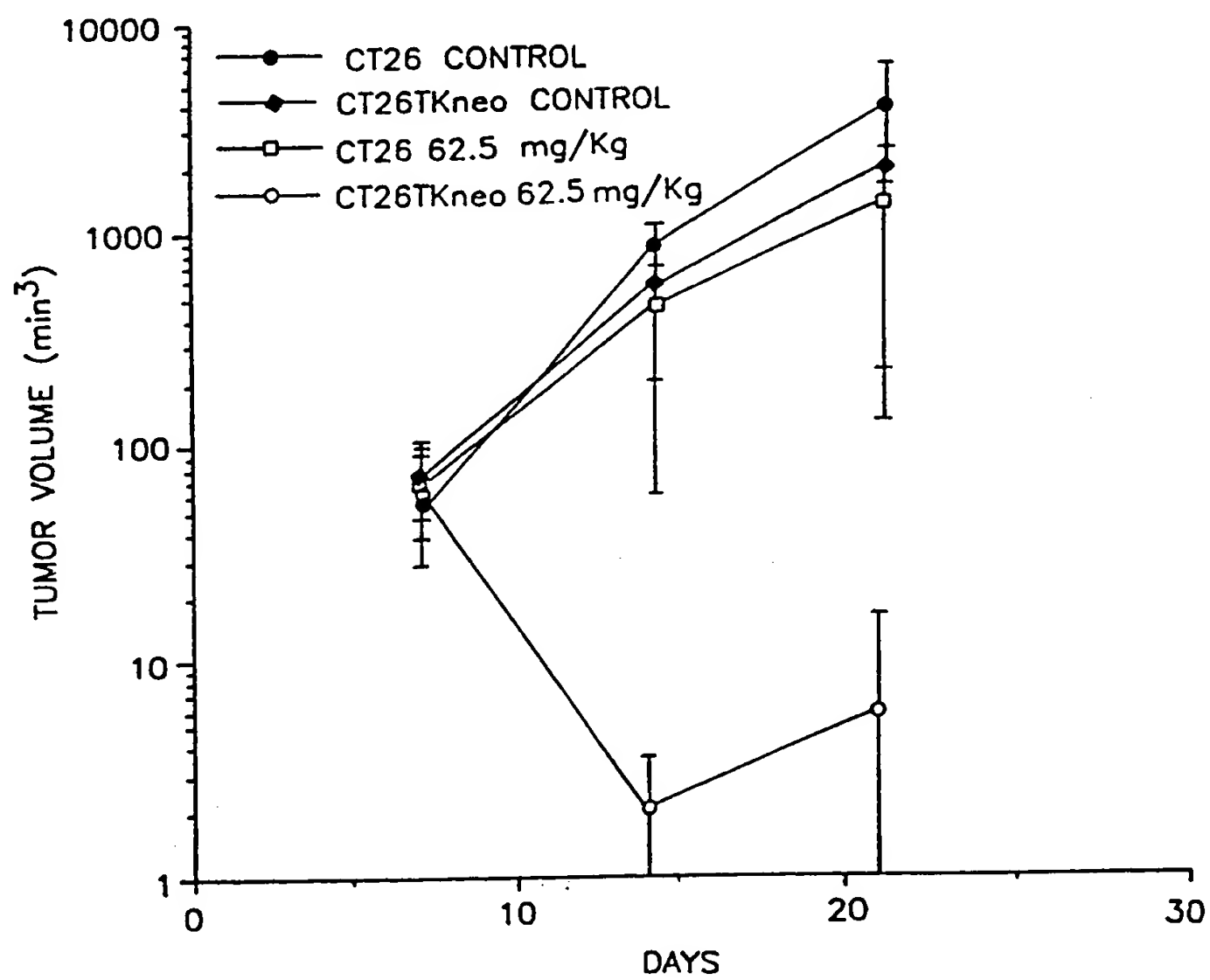
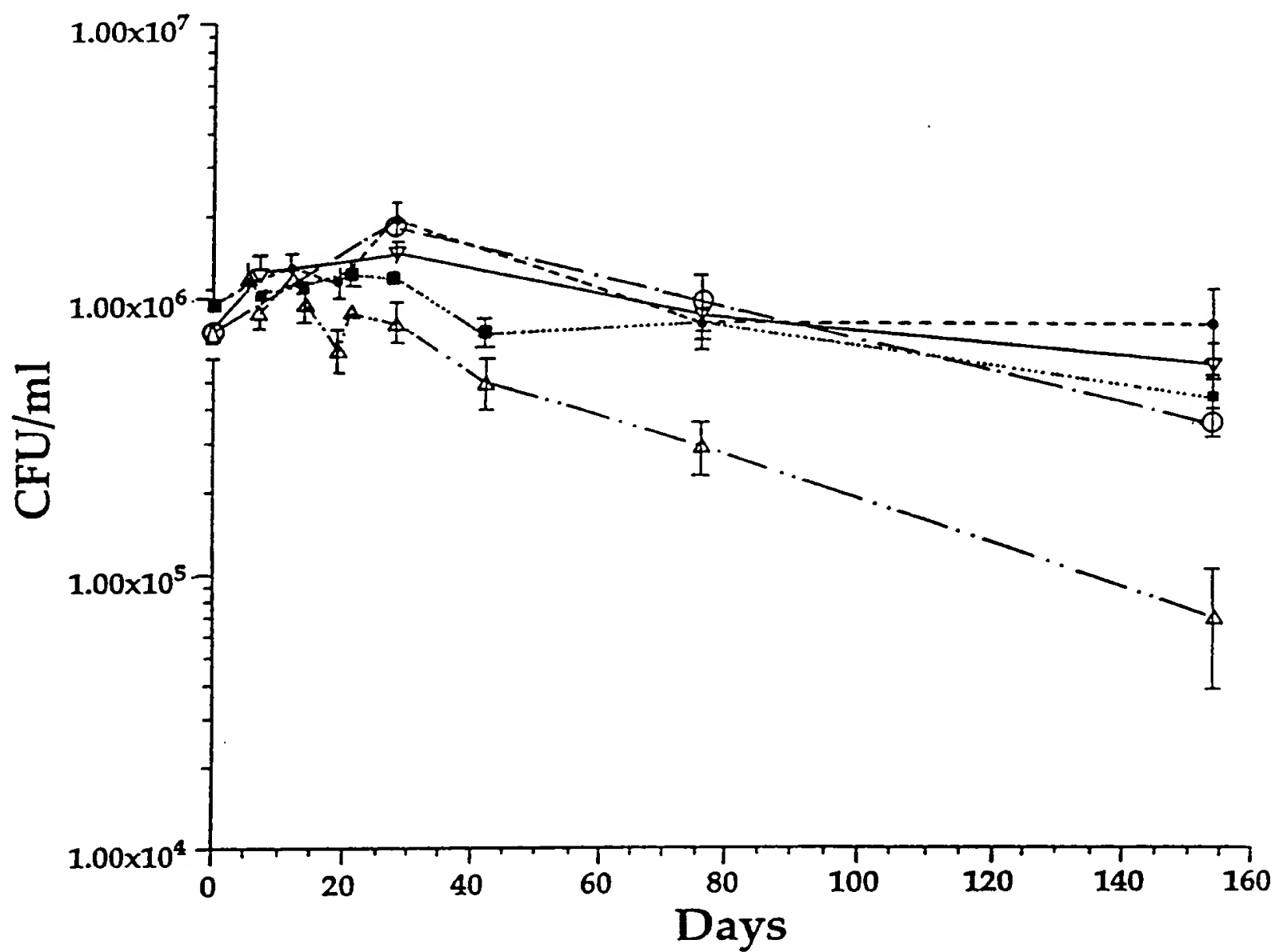


Fig 12



Formulation:

25mM Tris pH 7.2
 60mM NaCl
 1 mg/ml Arginine
 5 mg/ml HSA
 50 mg/ml Lactose

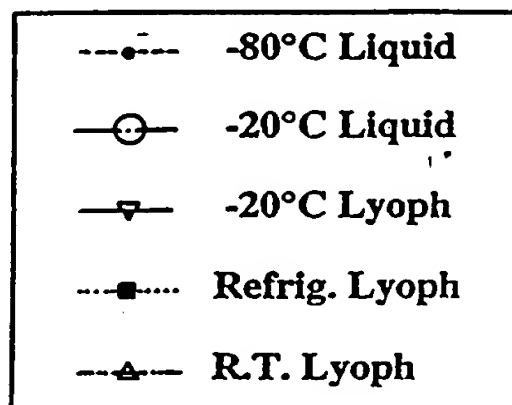
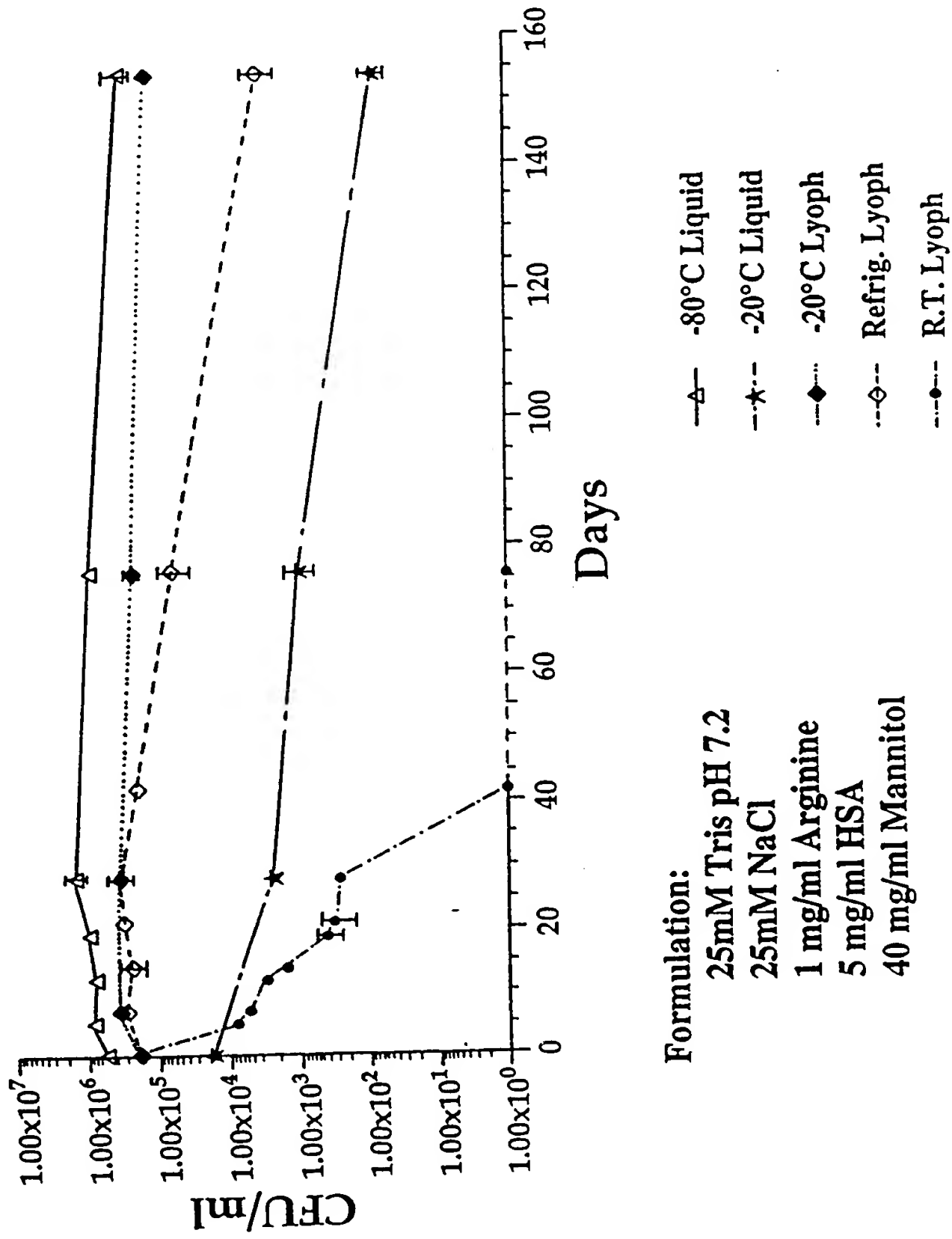
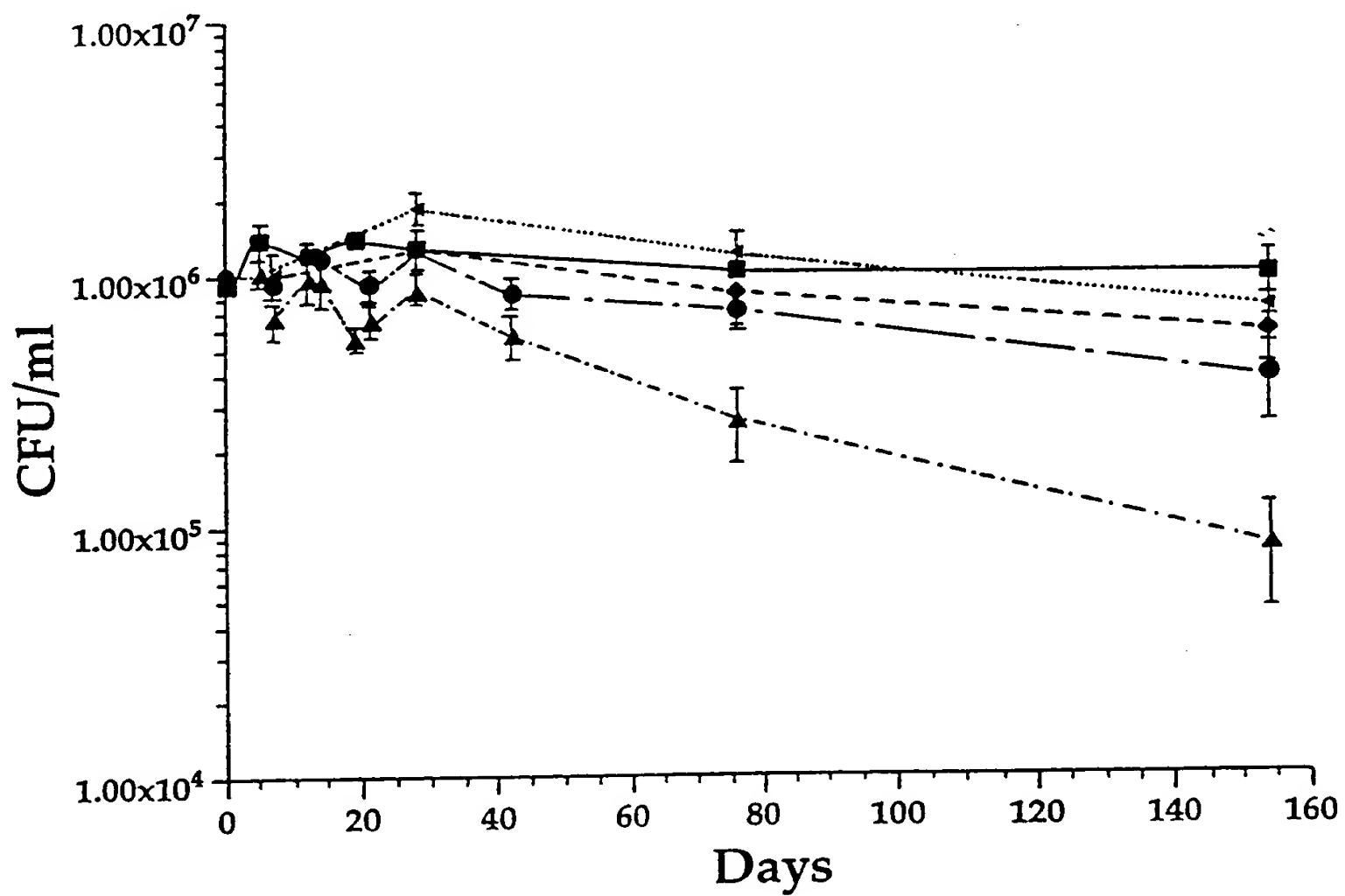


FIG. 13



Formulation:
 25mM Tris pH 7.2
 25mM NaCl
 1 mg/ml Arginine
 5 mg/ml HSA
 40 mg/ml Mannitol

FIG. 14



Formulation:

25mM Tris pH 7.2
 60mM NaCl
 1mg/ml Arginine
 5mg/ml HSA
 50mg/ml Trehalose

- -80°C Liquid
-△..... -20°C Liquid
- ◆--- -20°C Lyoph
- Refrig. Lyoph
- ▲— R.T. Lyoph

FIG. 15

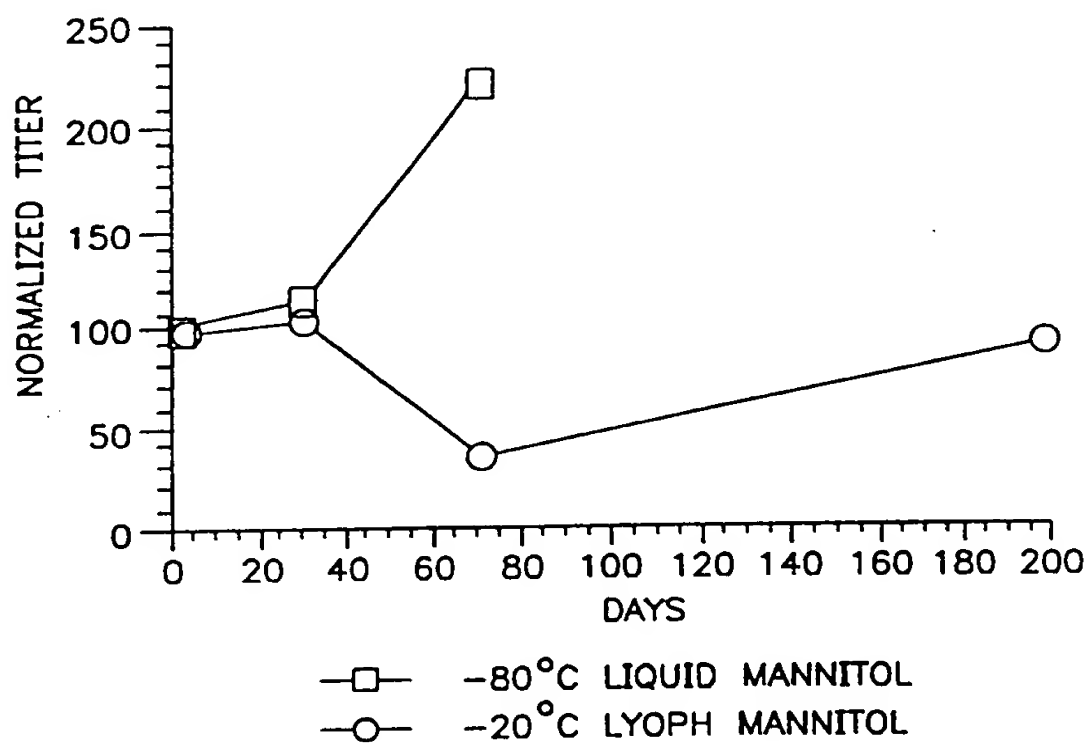


FIG. 16A

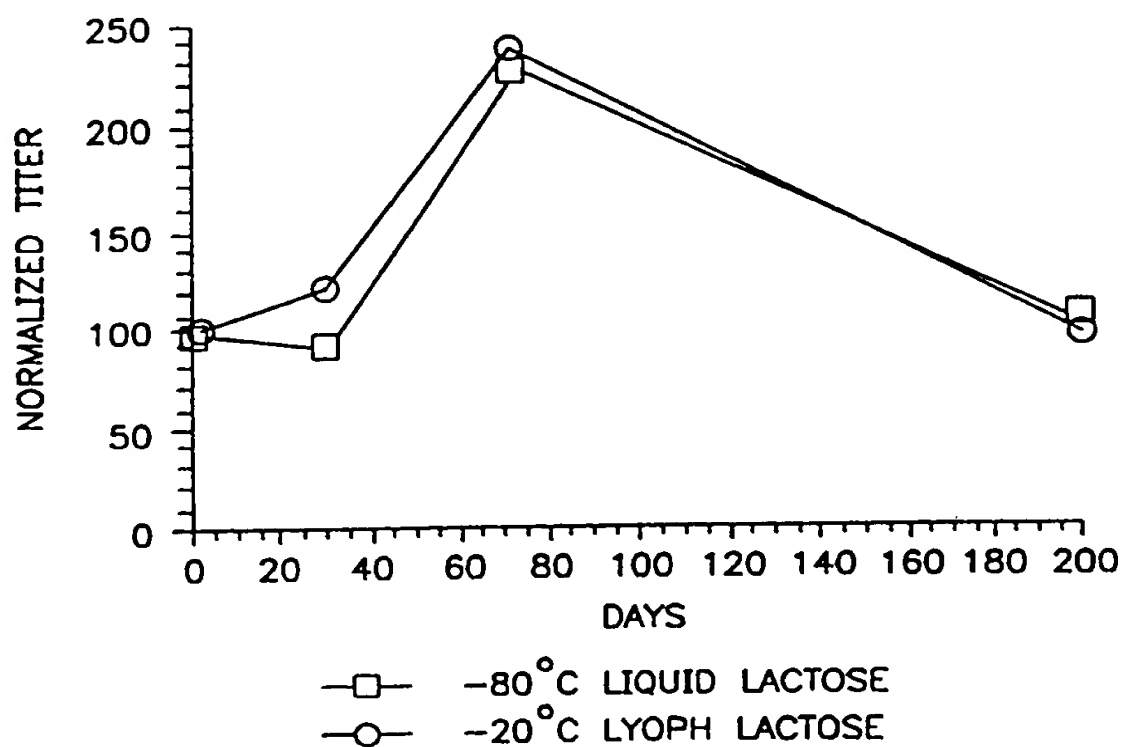


FIG. 16B

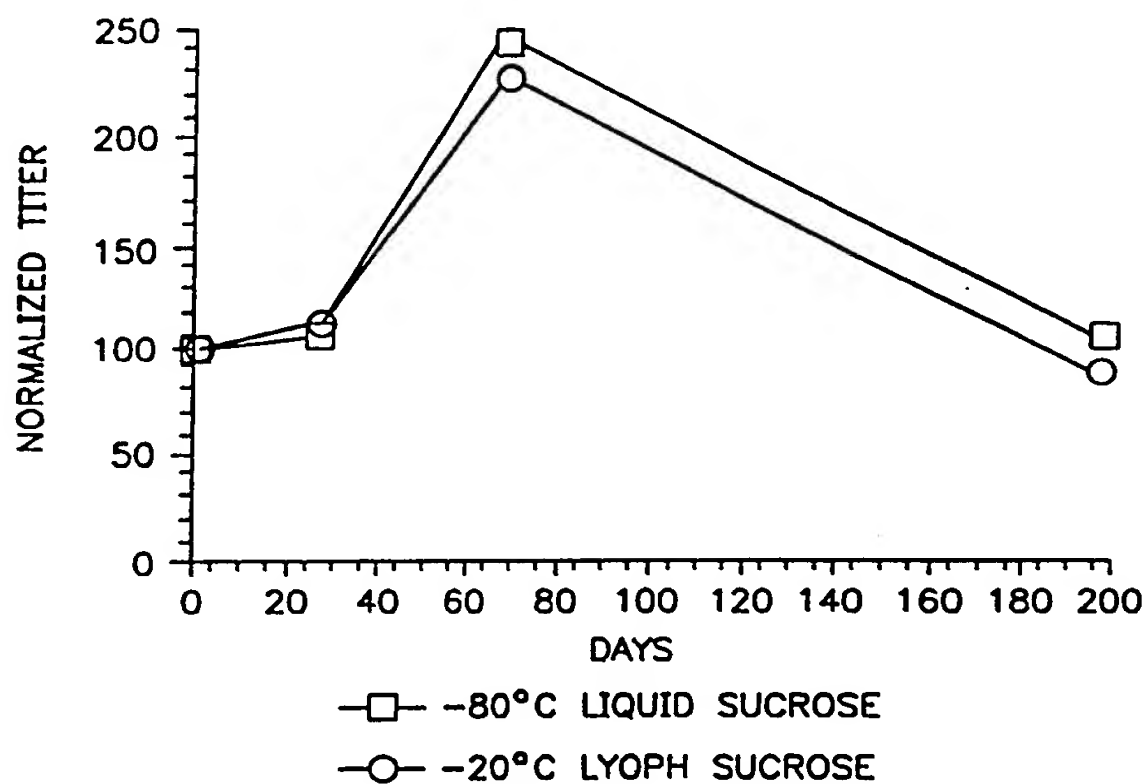


FIG. 16C

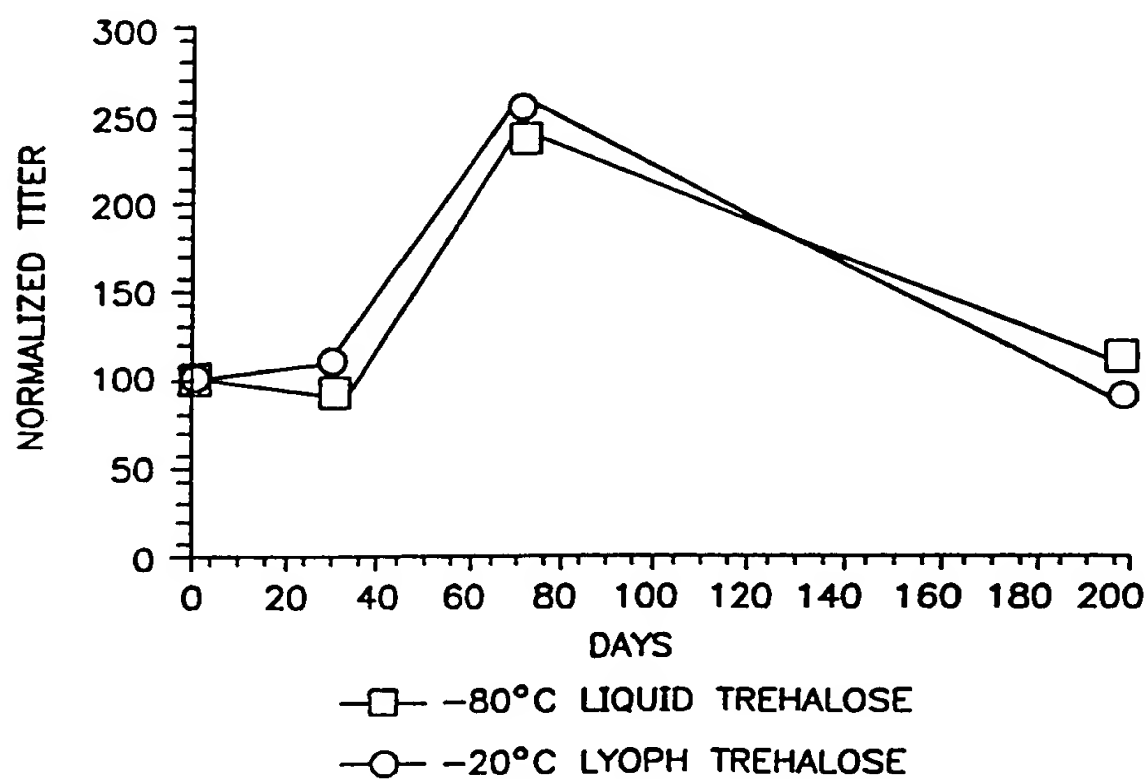


FIG. 16D

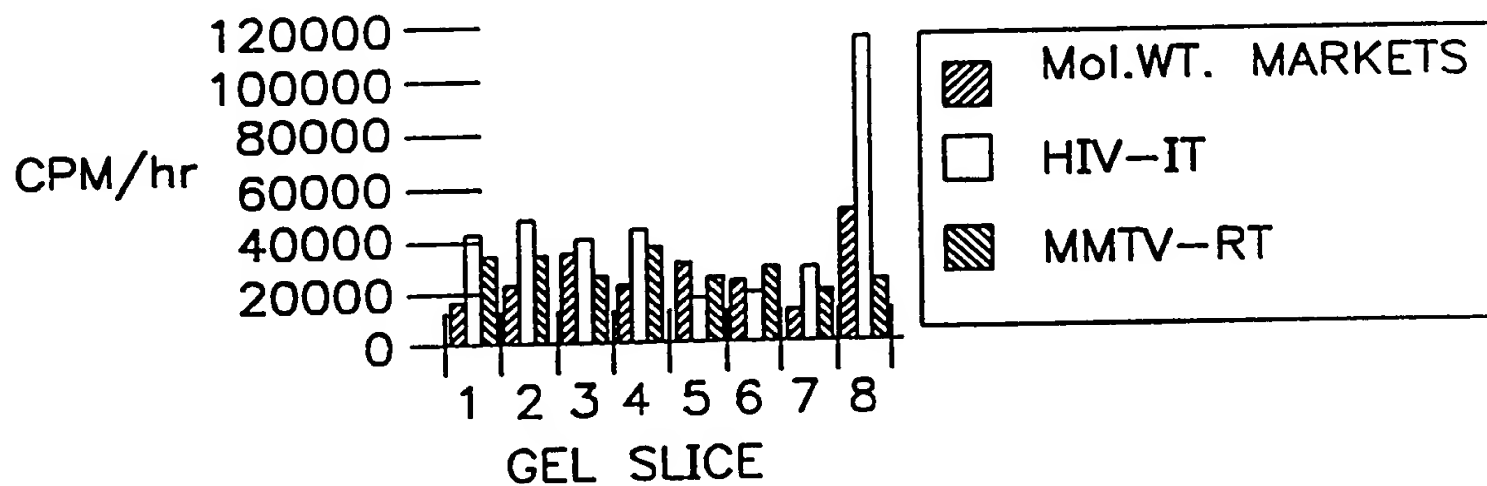


FIG. 17

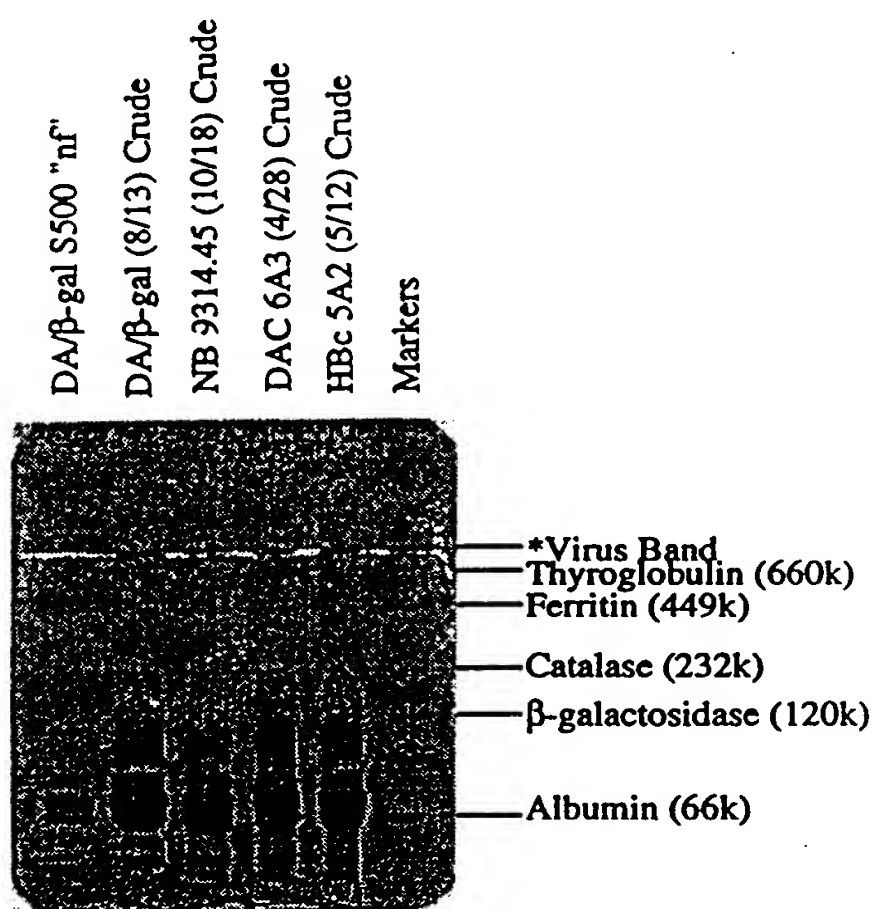


FIG. 18

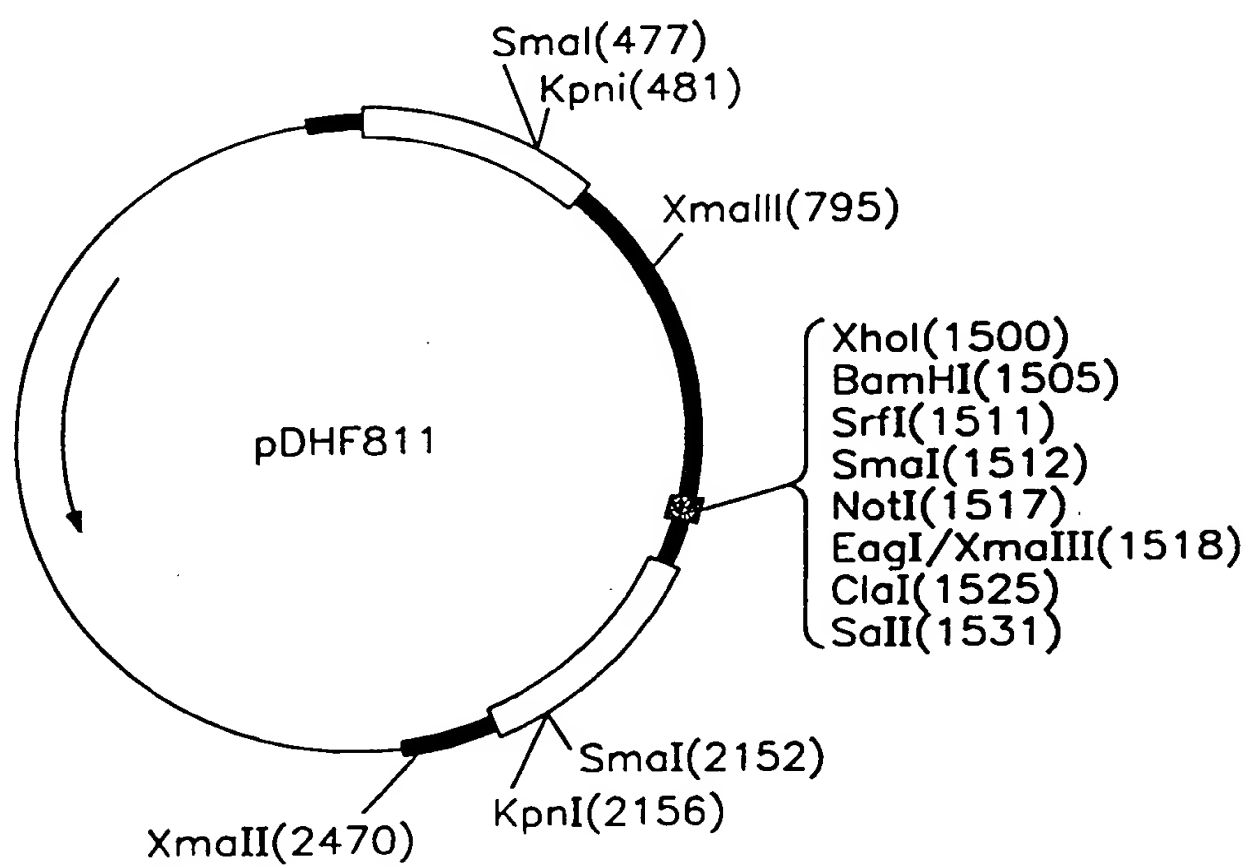


FIG. 19

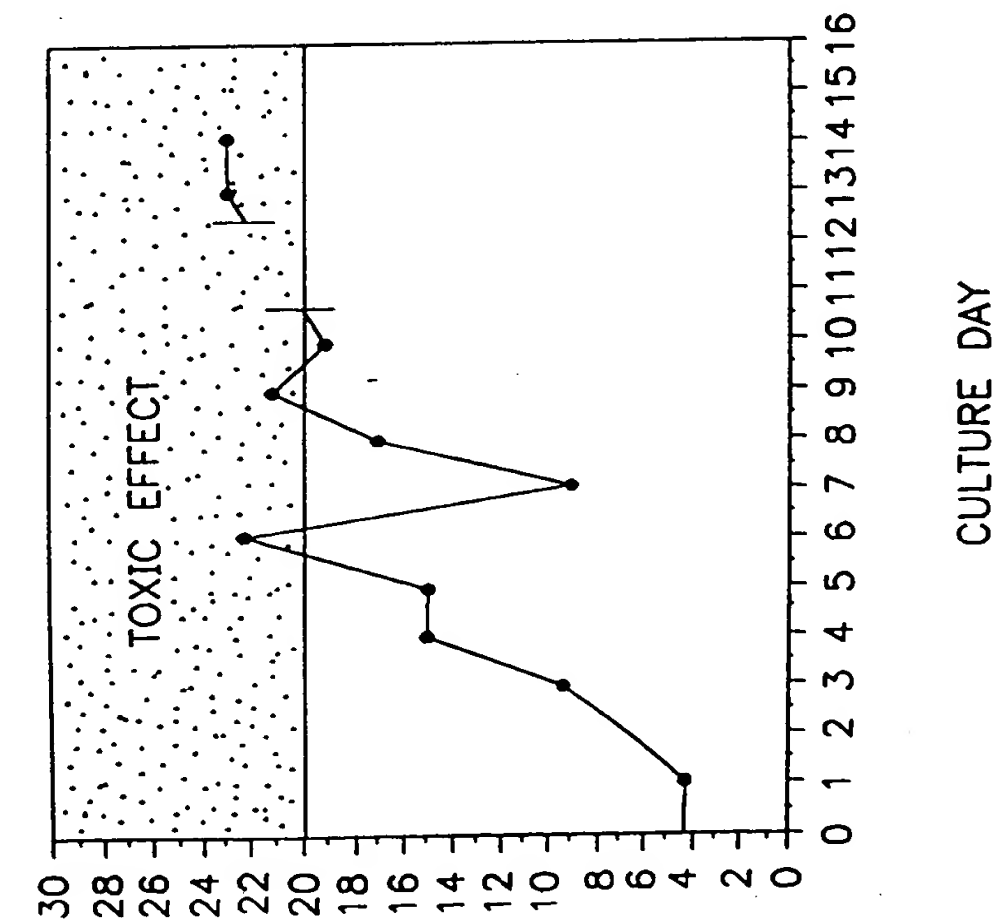


FIG. 20A

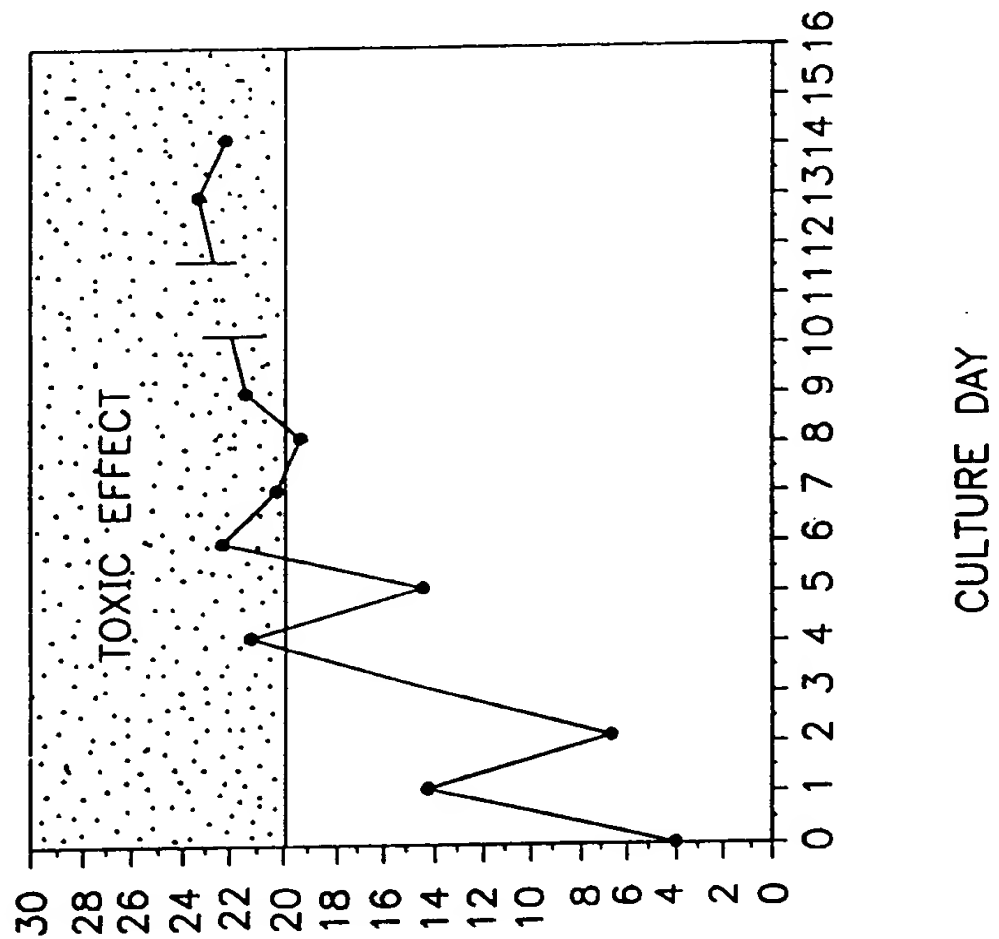


FIG. 20B

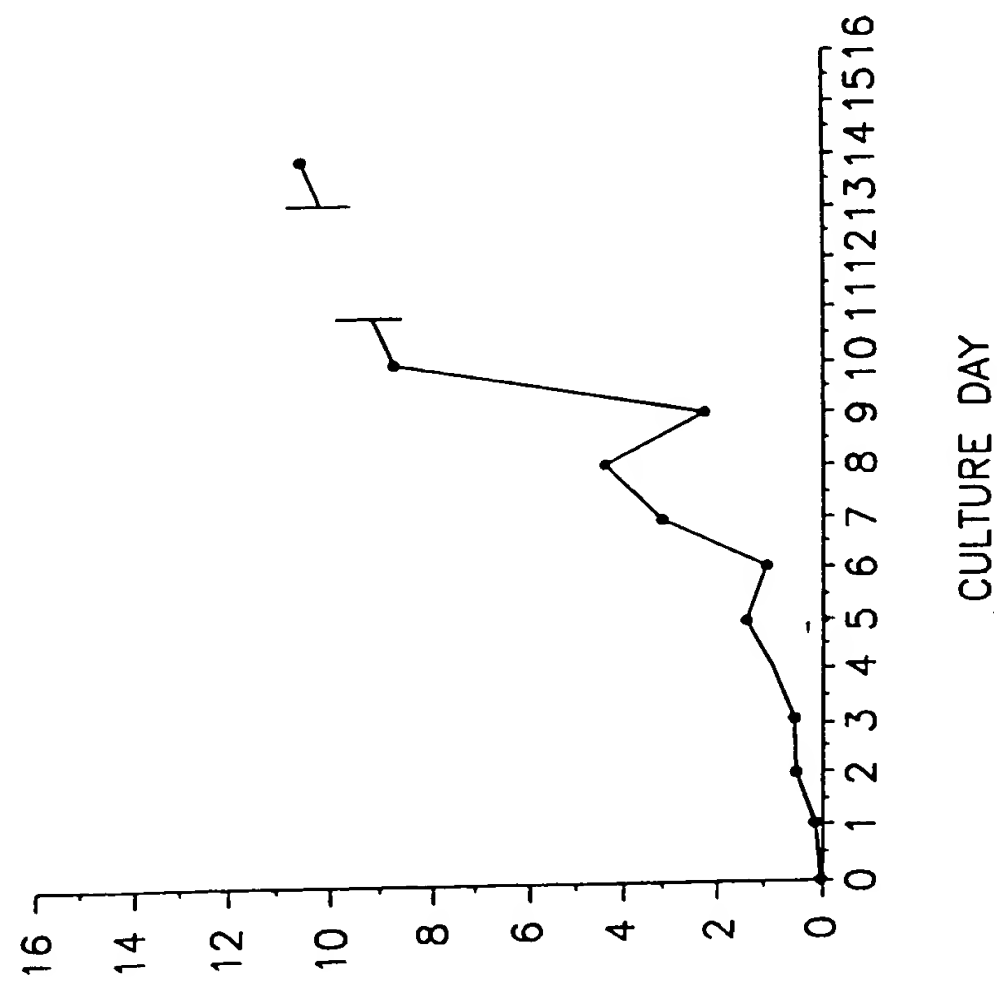


FIG. 20C

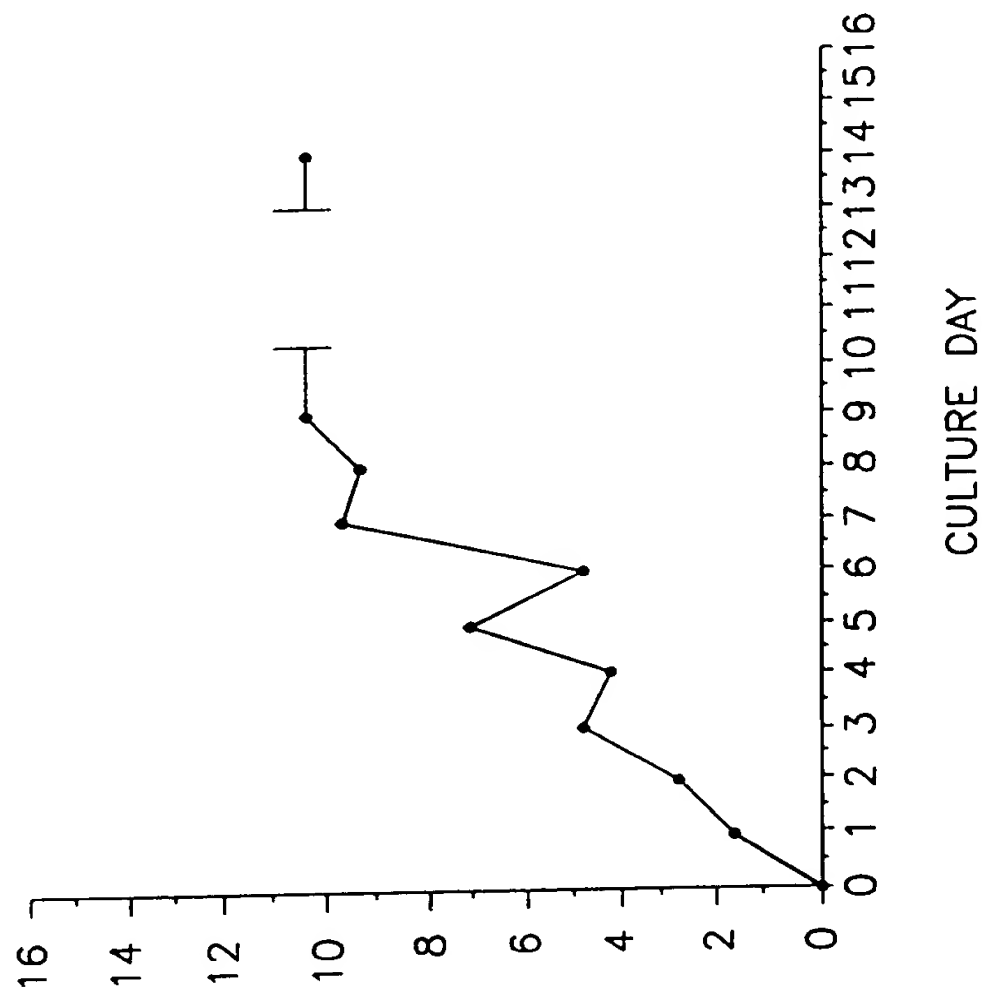


FIG. 20D

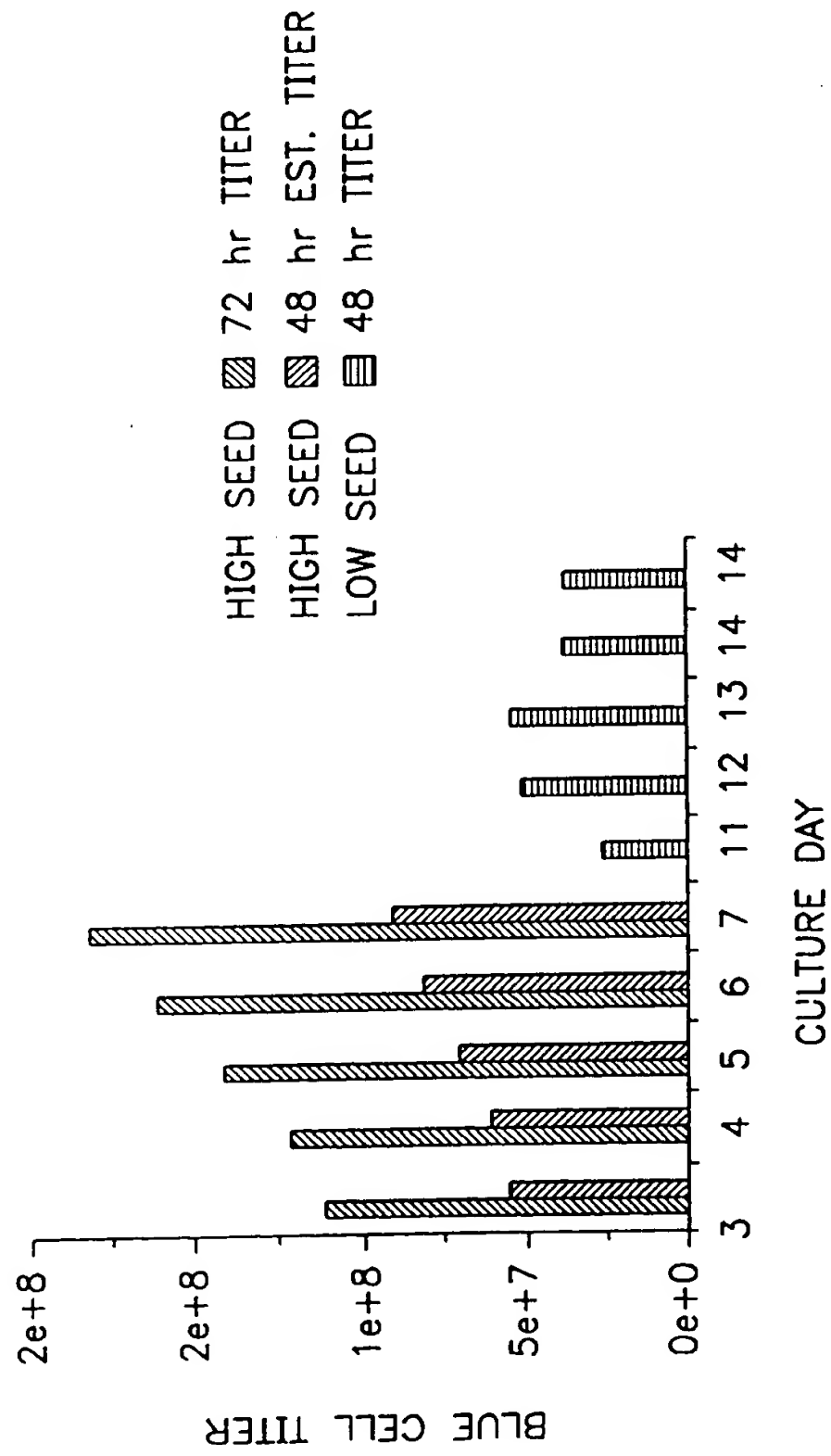
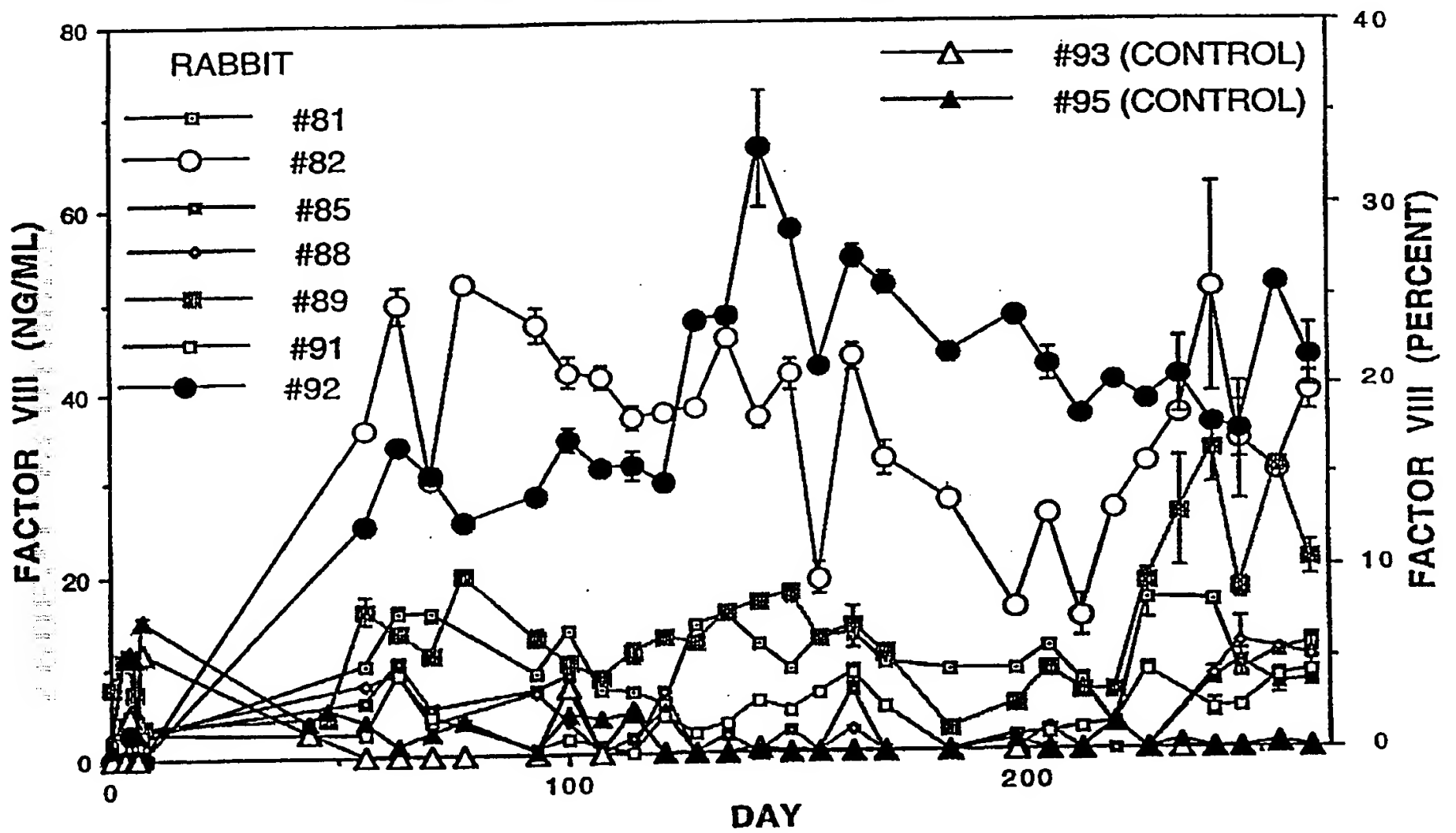


FIG. 21

Fig 22

P614.8 FACTOR VIII RABBITS



FACTOR VIII EXPRESSION IN RABBITS

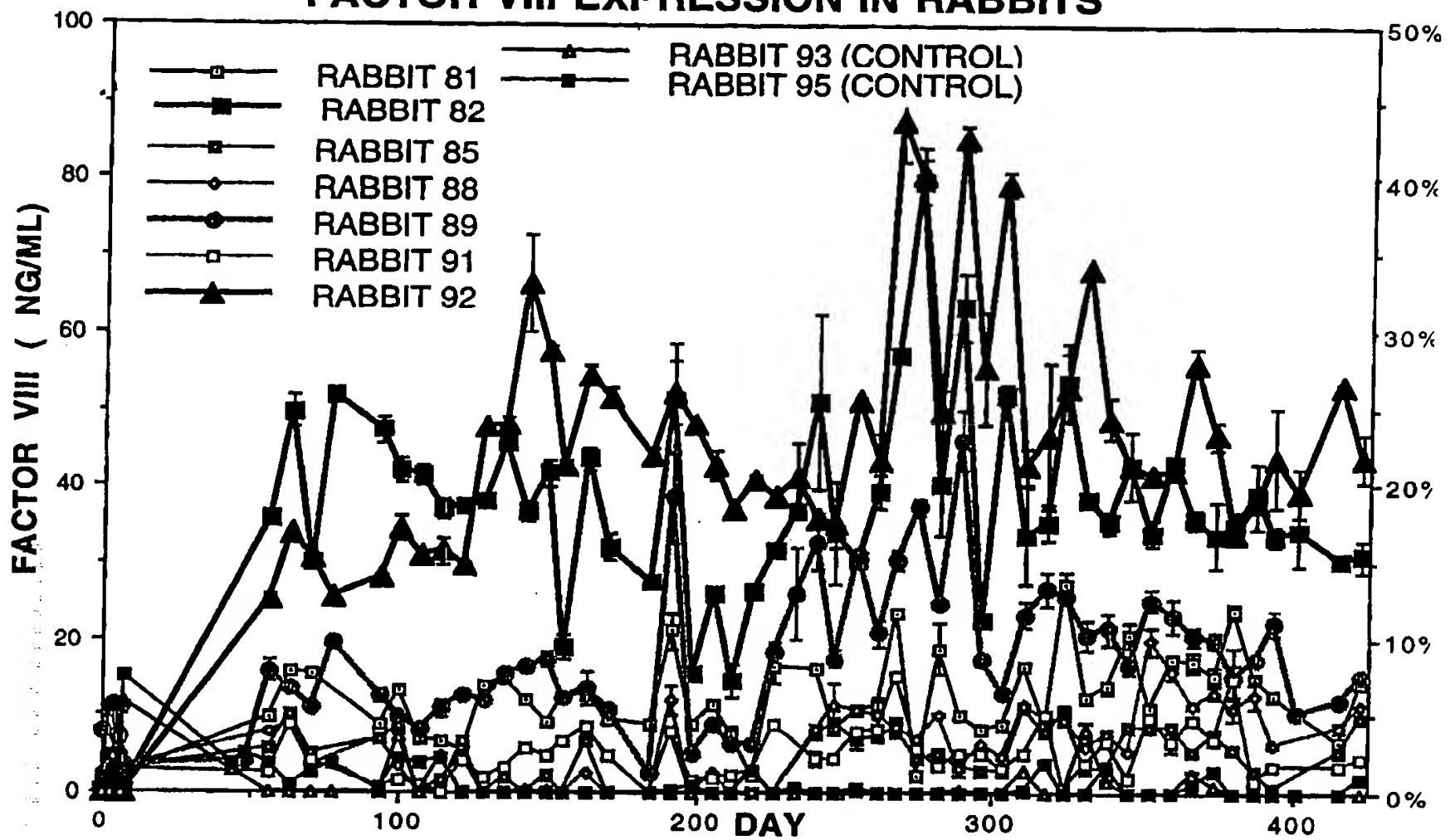


Fig 23

SYSTEMIC HUMAN GROWTH HORMONE EXPRESSION IN RABBITS

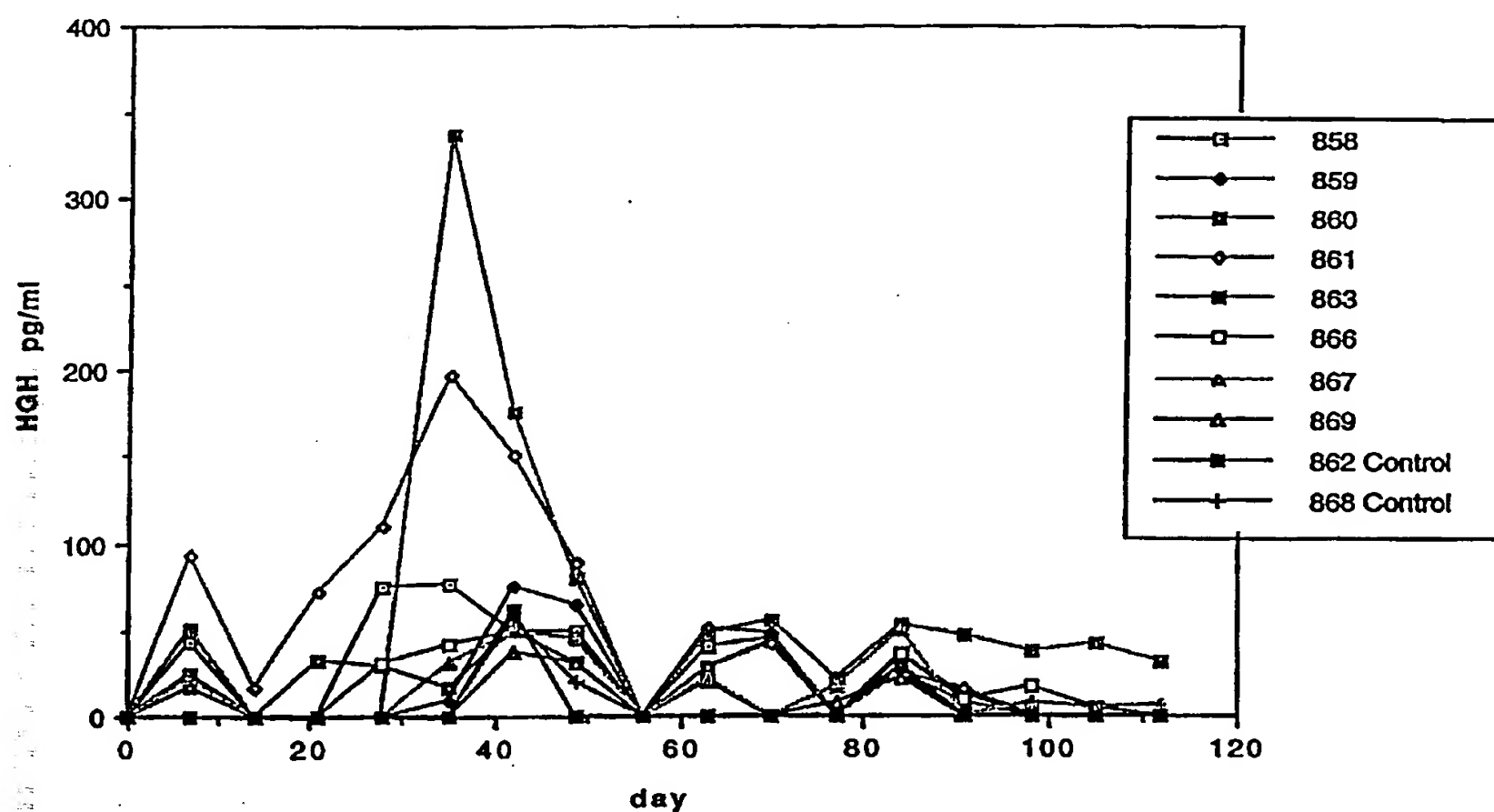
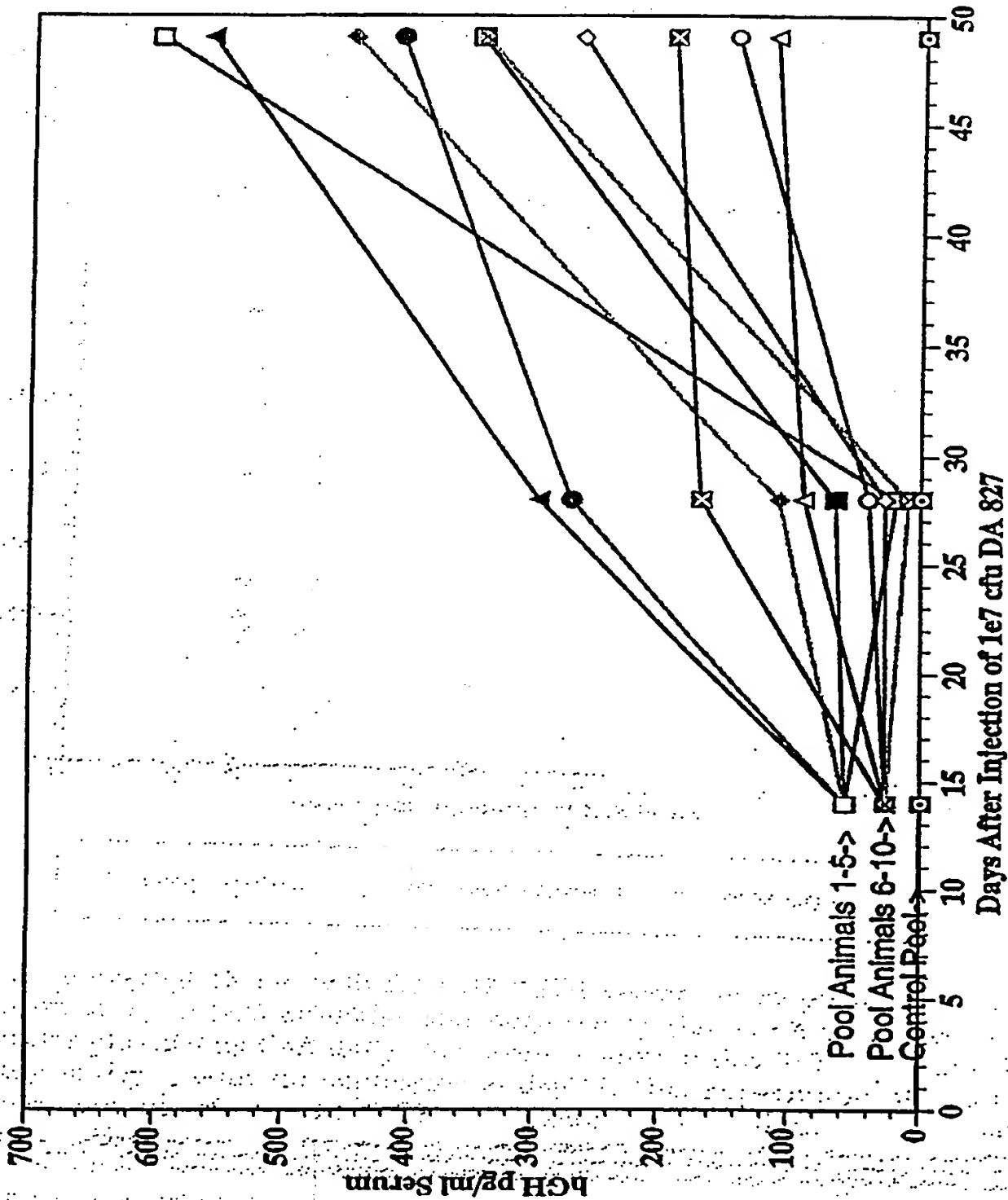


Fig 24

Time Course of hGH Expression in Mice Injected with DA 827

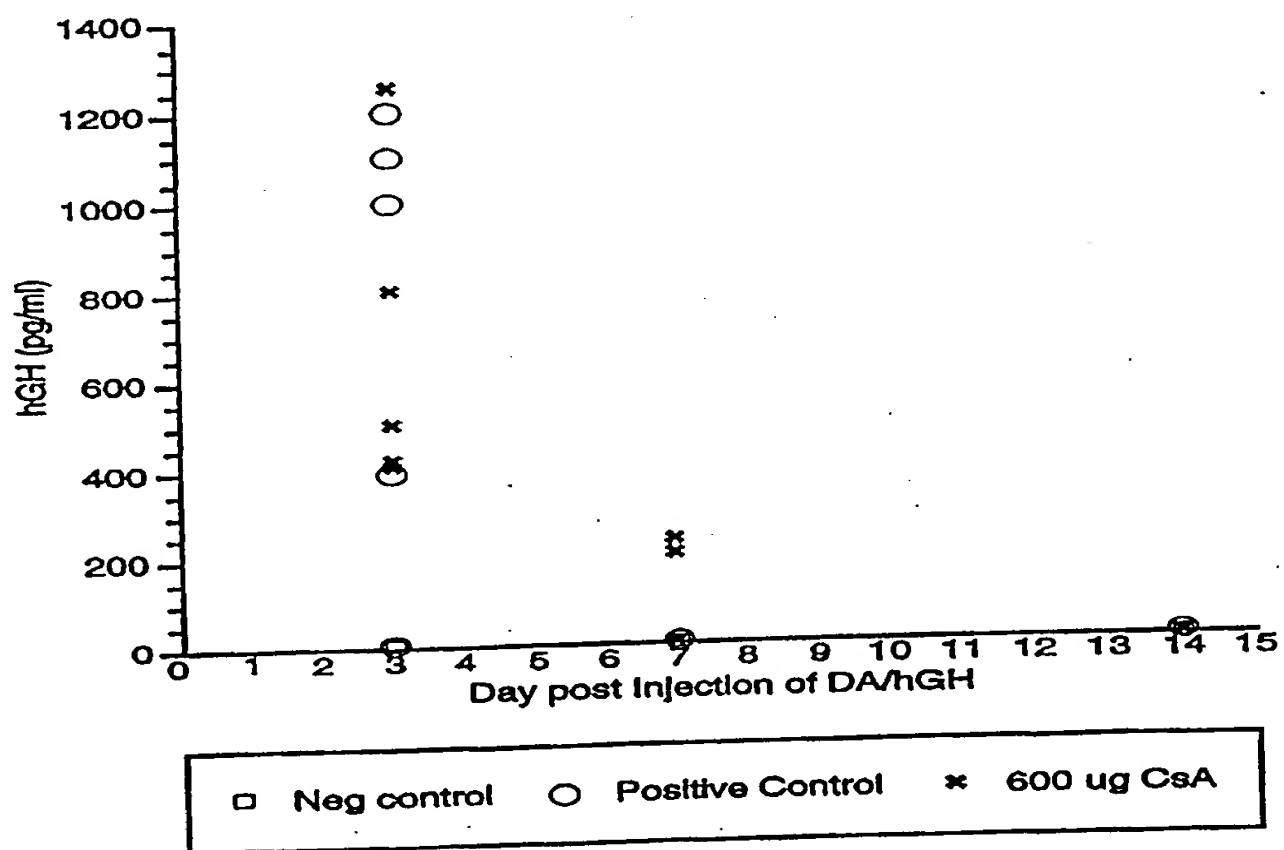


Time Point 1 (Day 14) is an average of each pool.

Fig 25

Fig 26

hGH Levels in Murine Sera



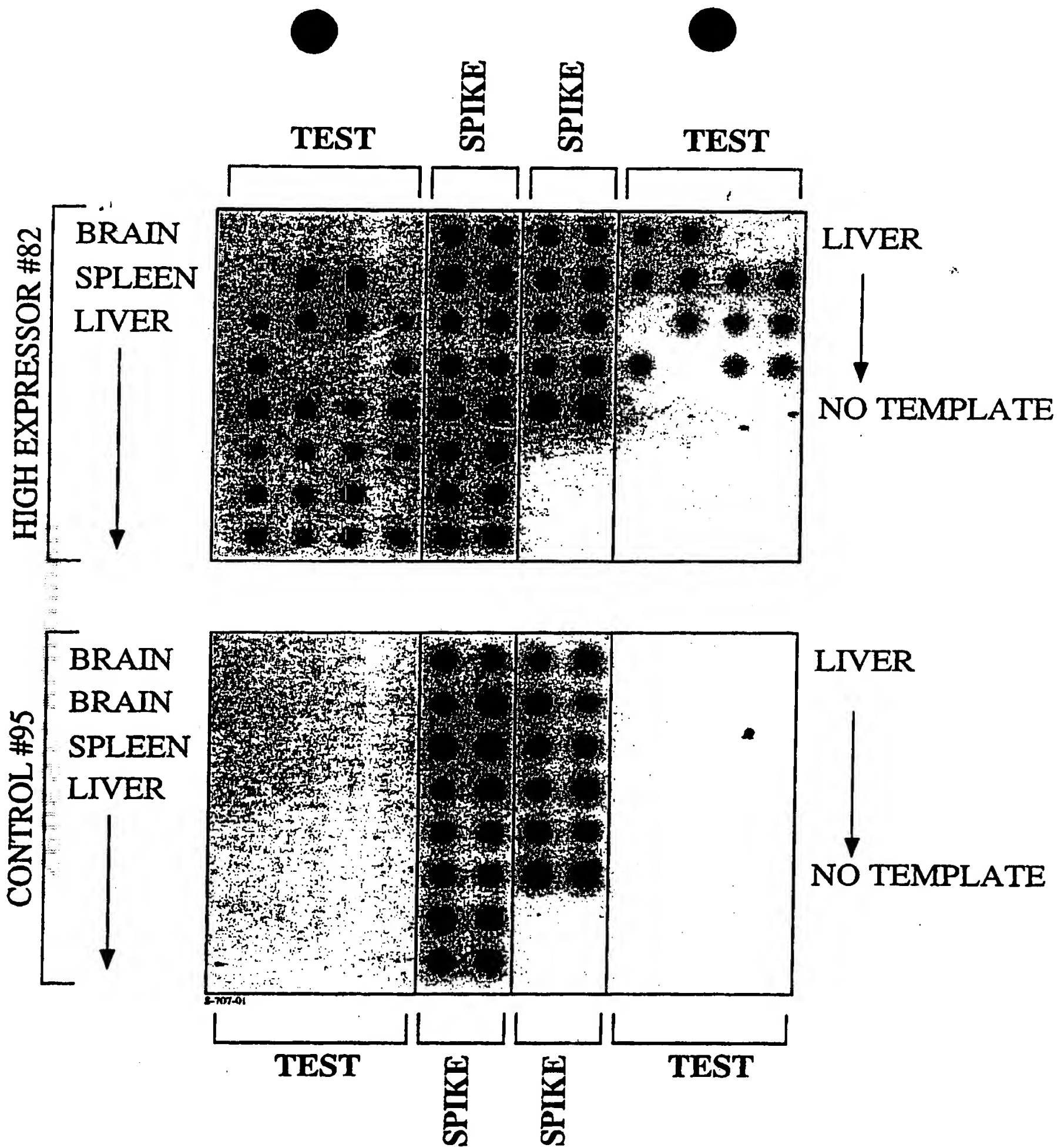


Fig 27

HUMAN GROWTH HORMONE PCR OF MOUSE TISSUE

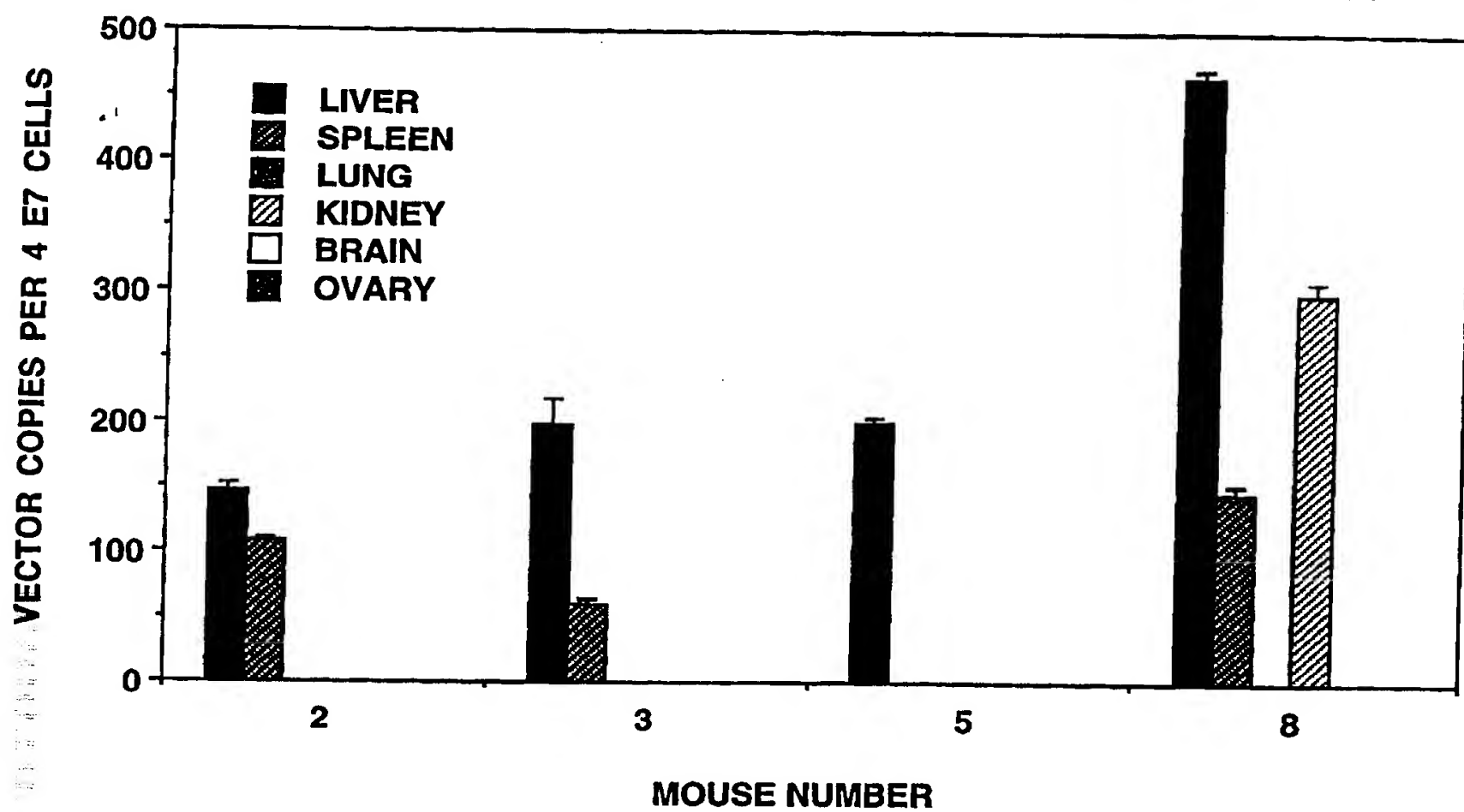


Fig 28

EXPRESSION OF HGH PROTEIN IN MOUSE ORGAN LYSATES

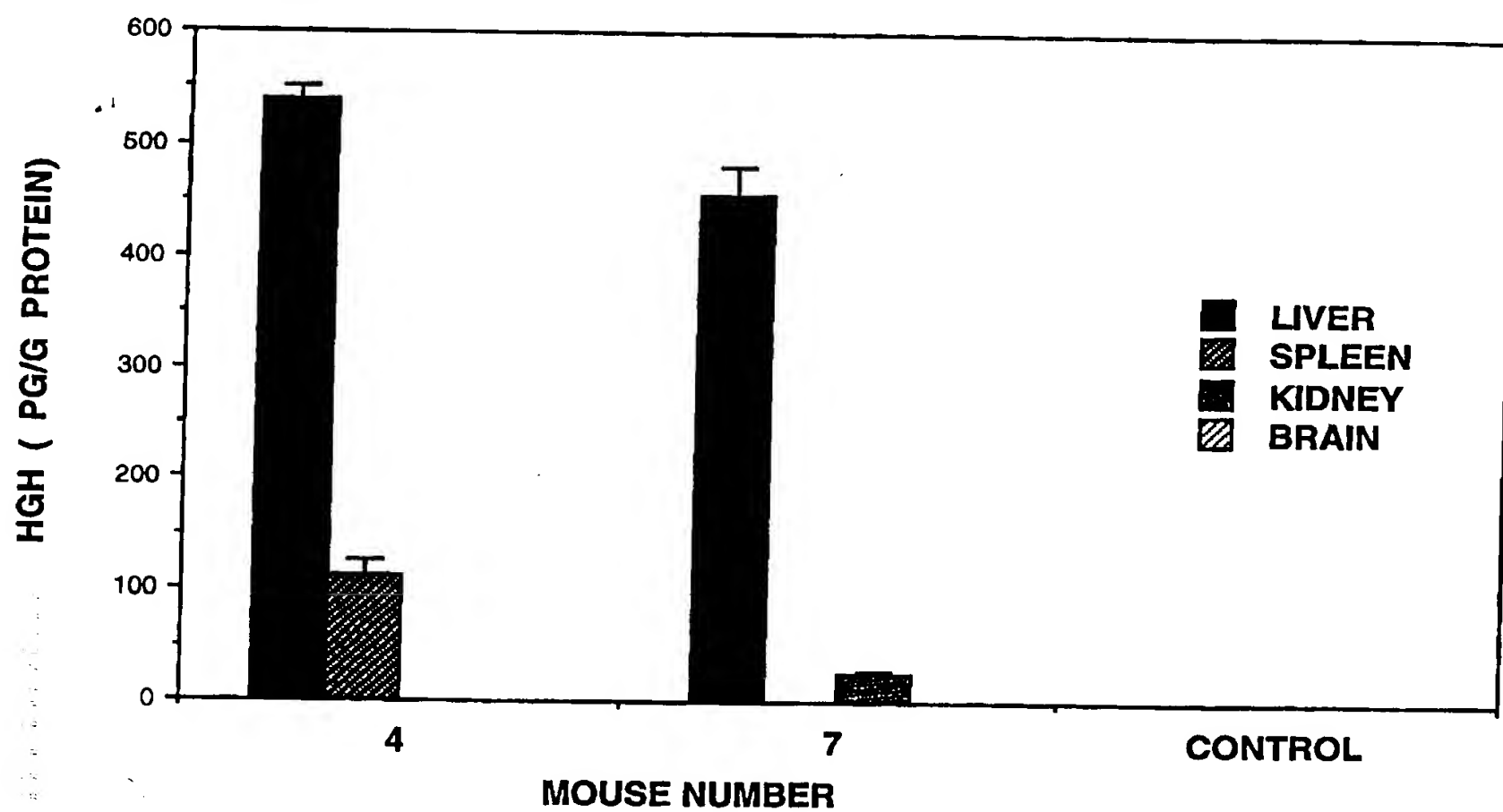


Fig 29

P888 NORMAL DOGS

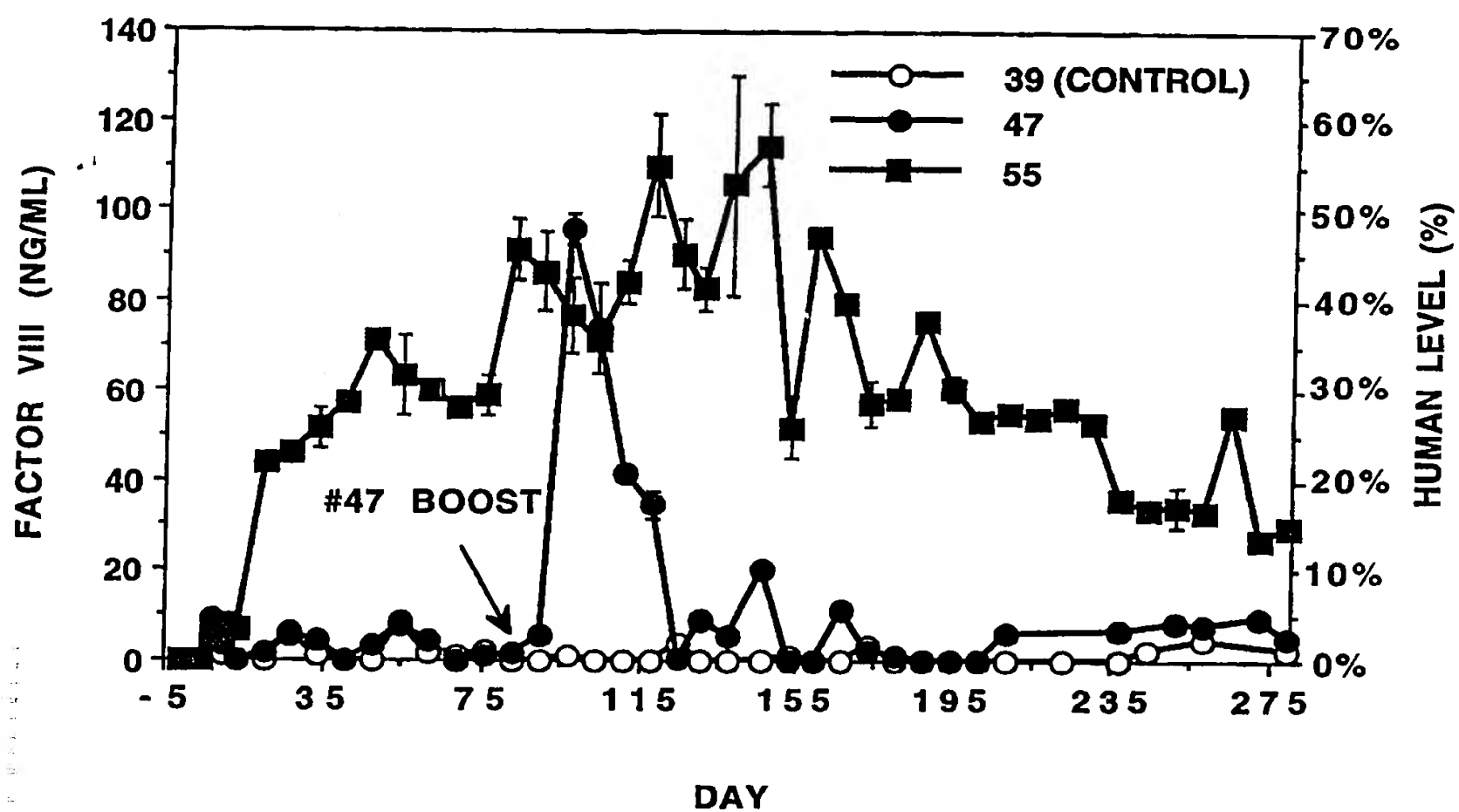


Fig 30

Transfer of hGH Expression by Spleenocytes

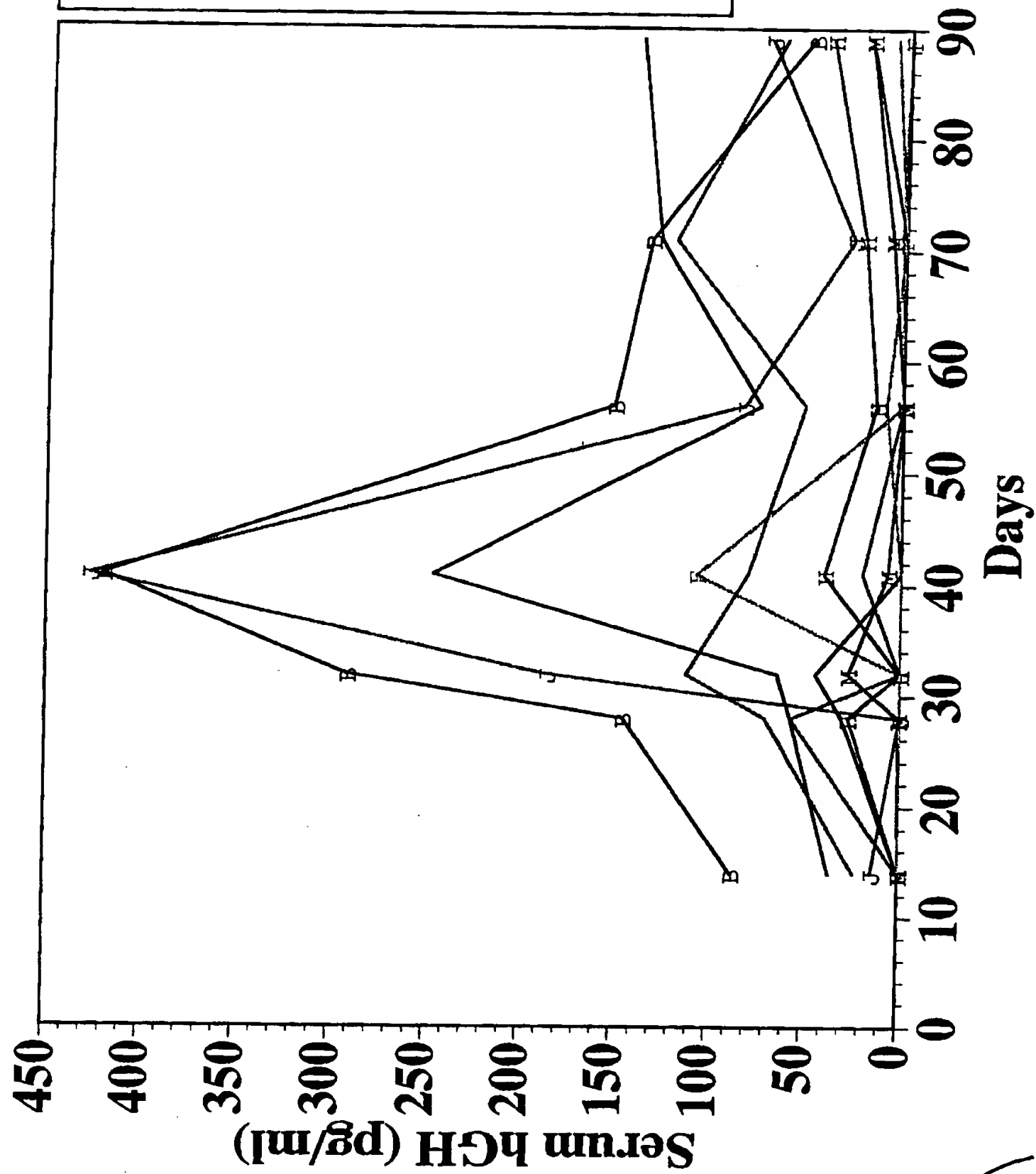


Fig 31

HEMOPHILIAC DOGS

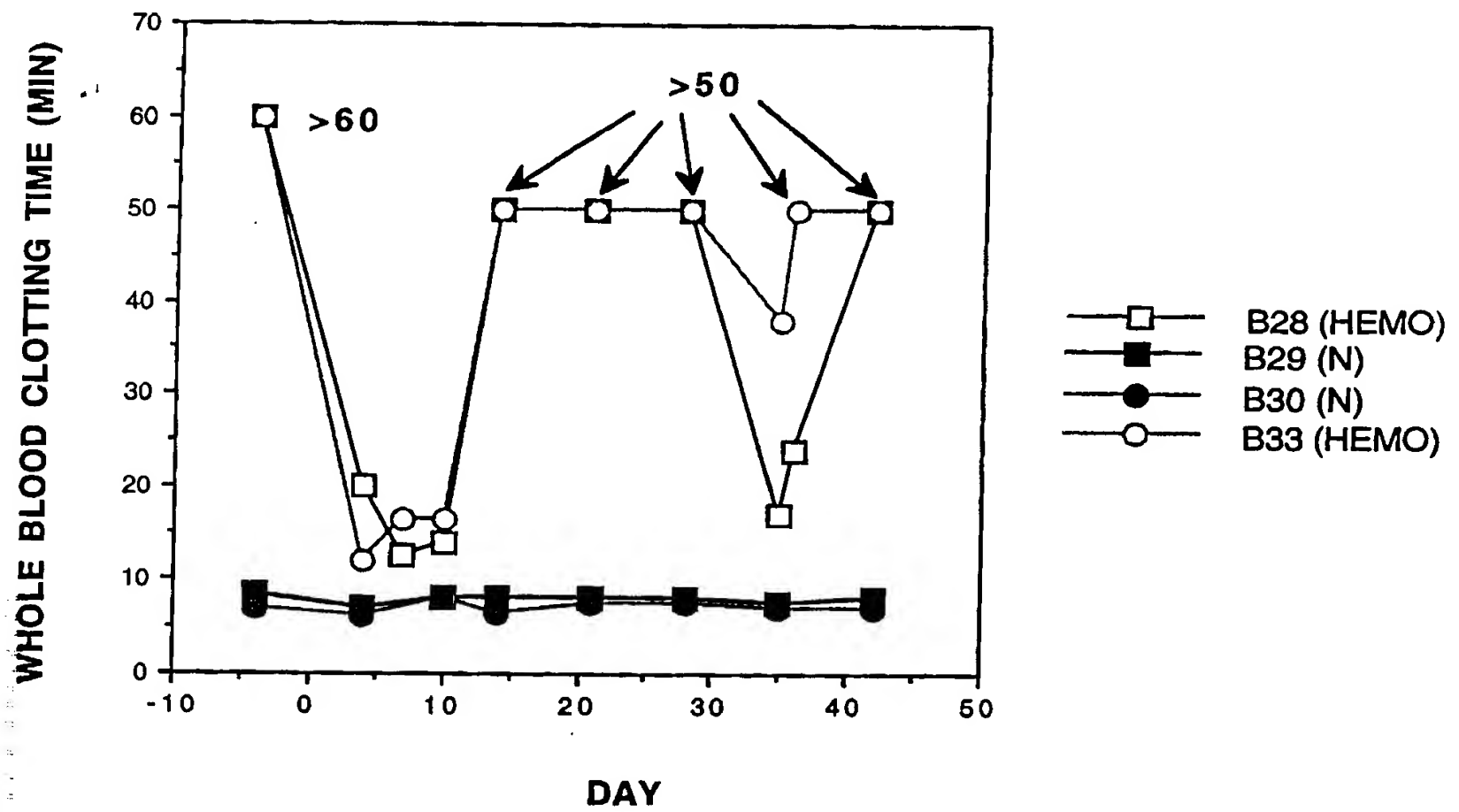


Fig 32

pKT1

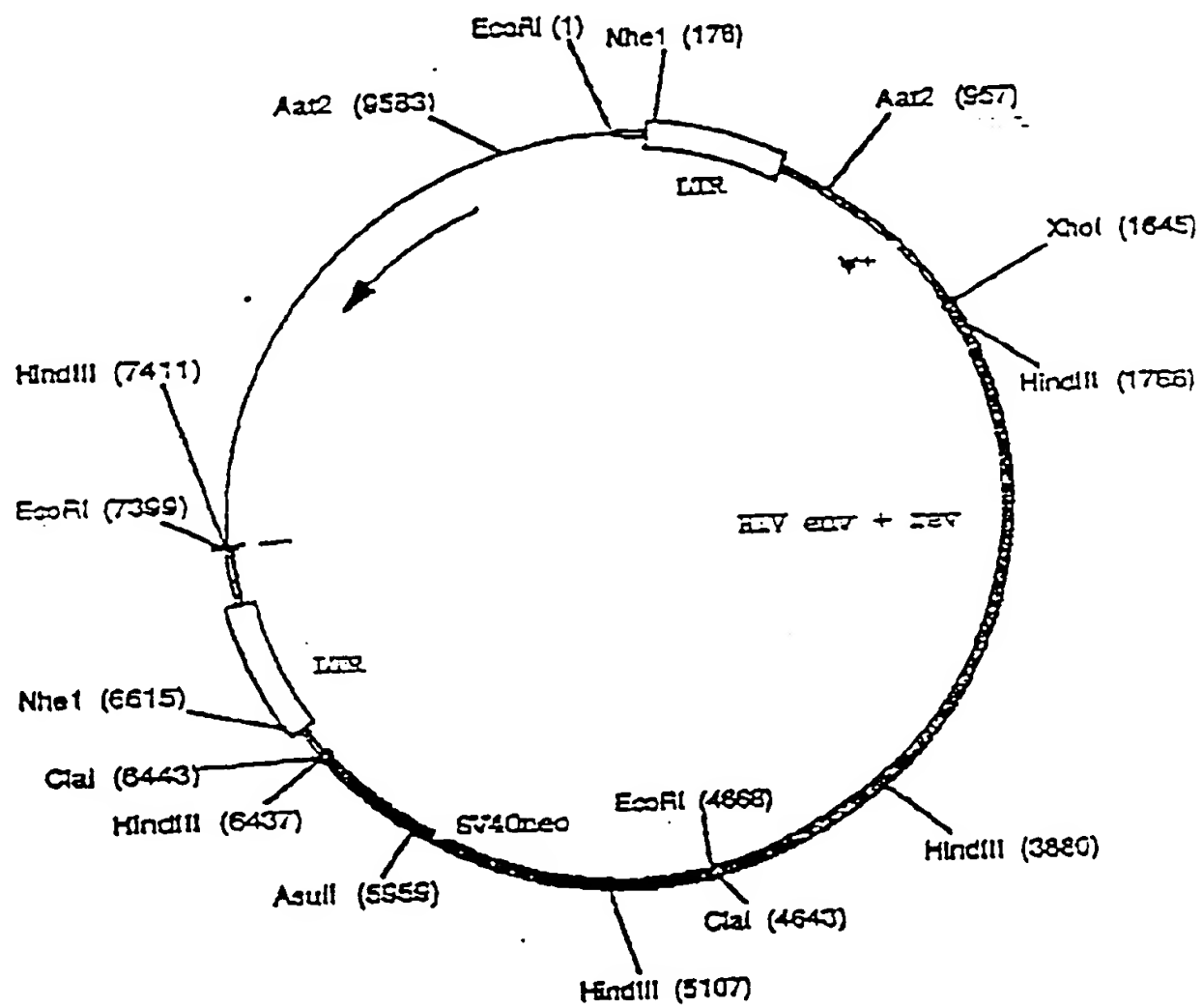
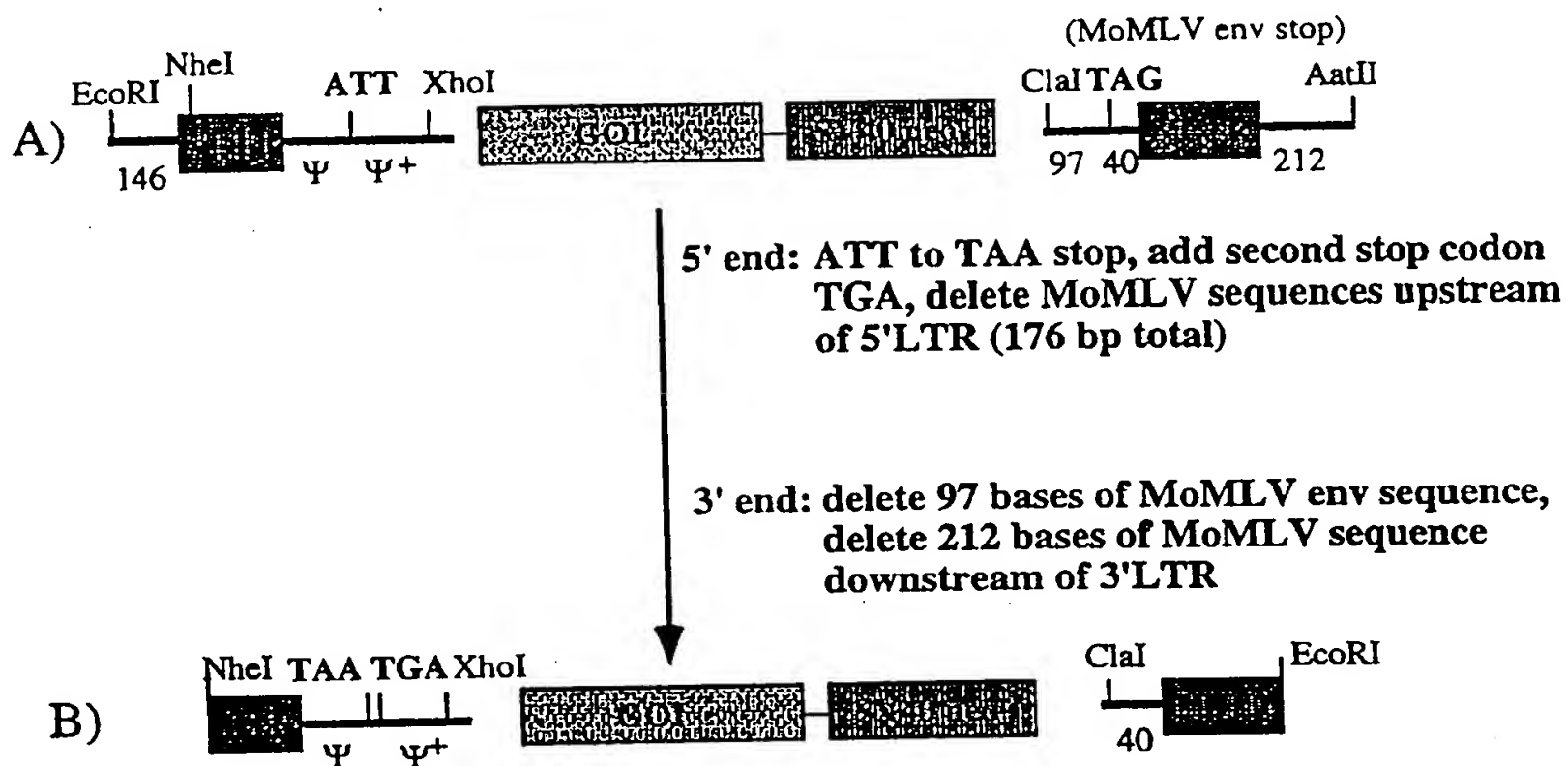


Fig 33

Fig 34

RETROVIRAL BACKBONE (N2-derived)



CROSS-LESS RETROVIRAL BACKBONE: pBA-5

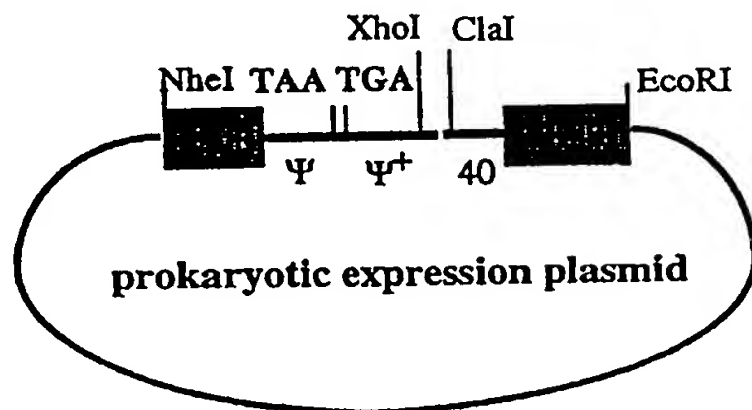


Fig 35

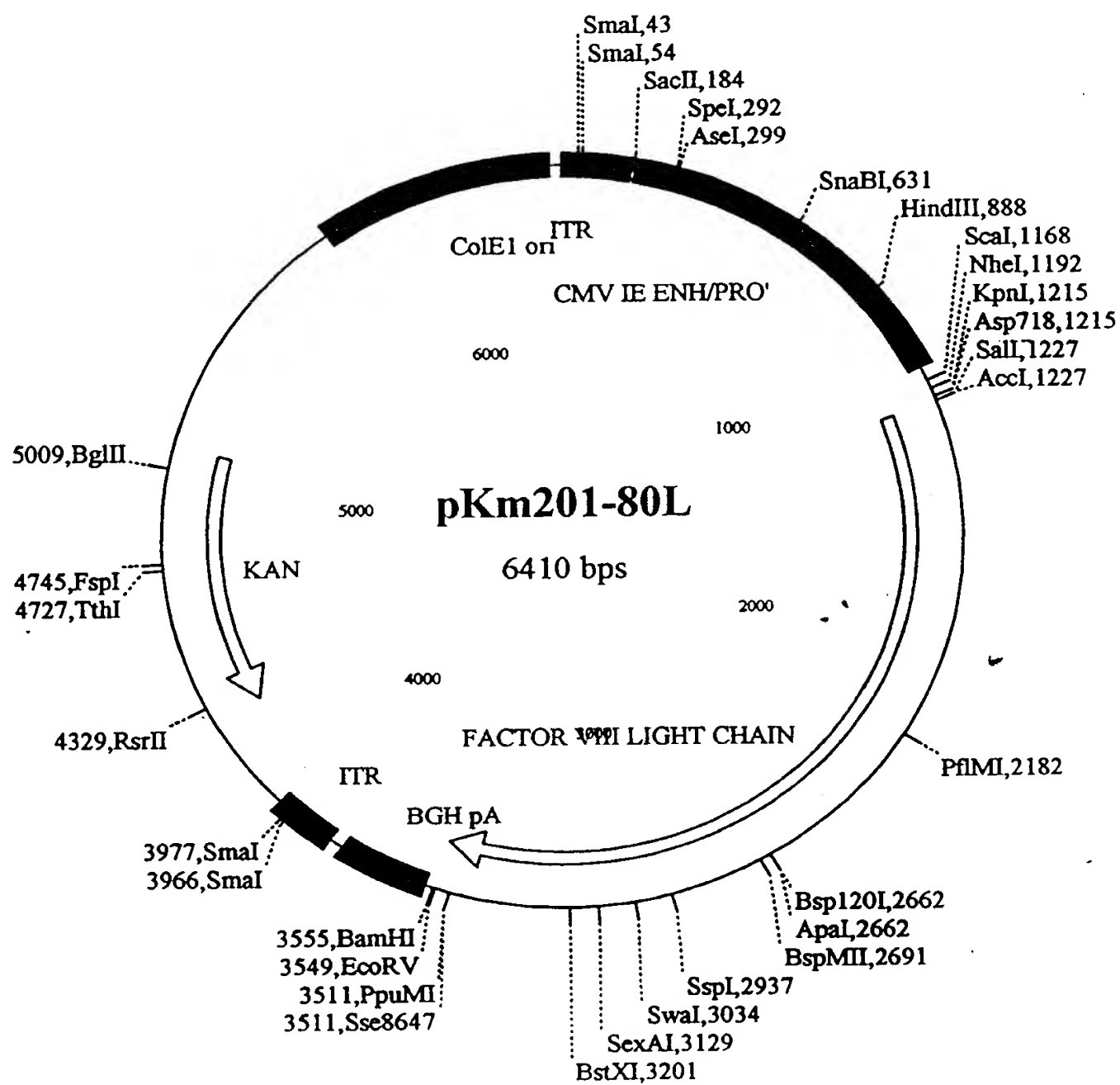


Fig 36

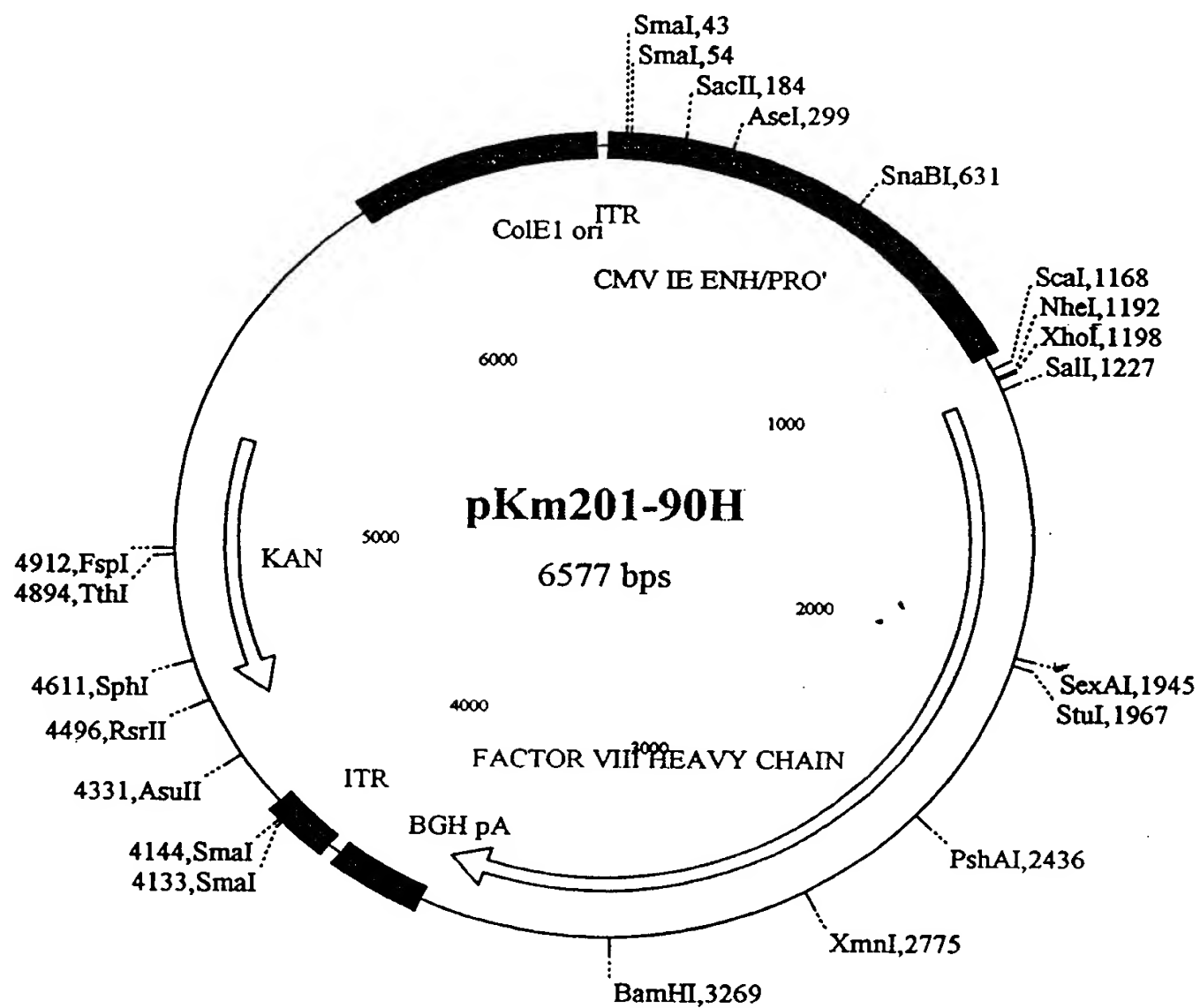
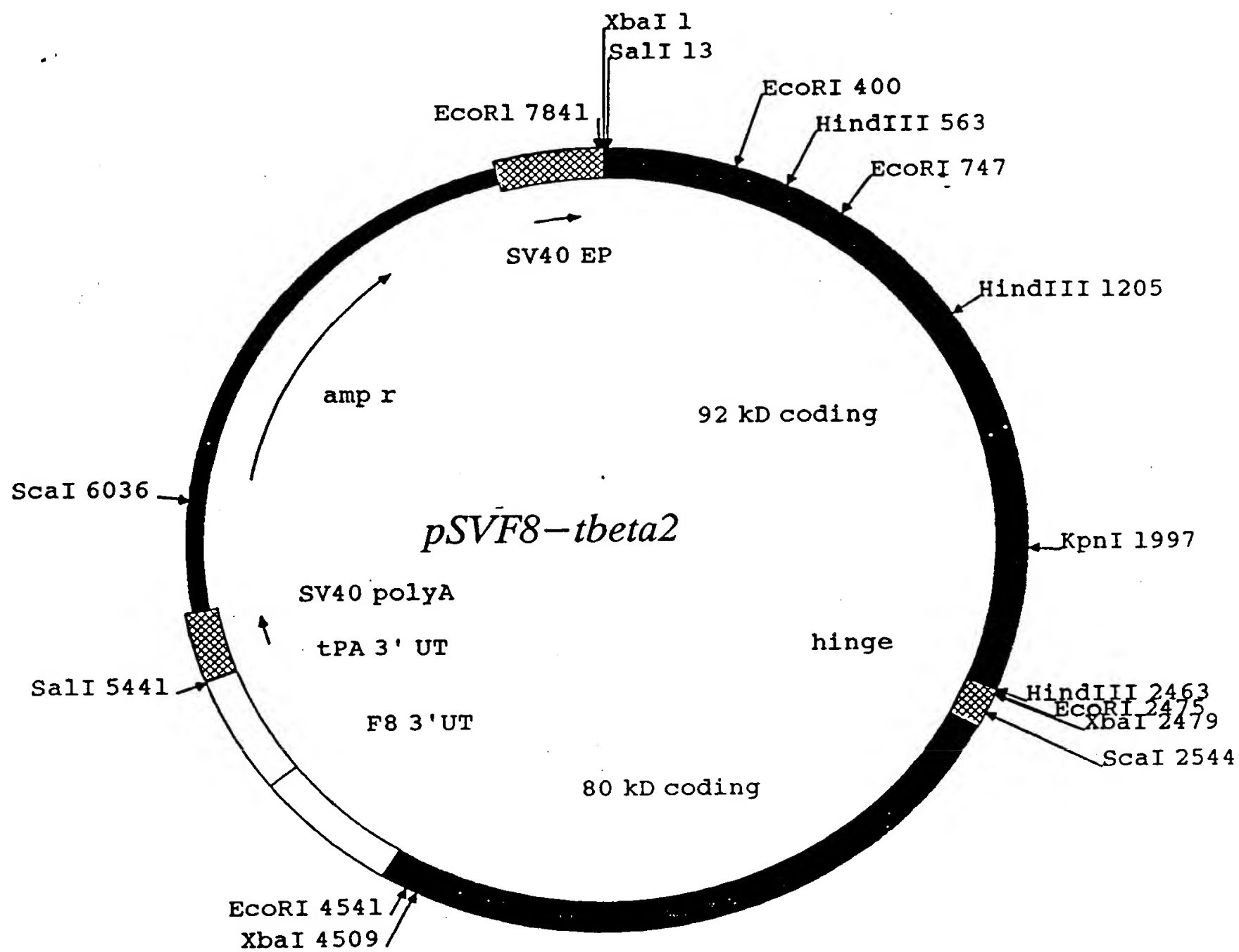


Fig 37



2341 ArgGlyMetThrAlaLeuLeuLysValSerSerCysAspLysAsnThrGlyAspTyrTyr Seq ID No. 48
AGAGGCATGACCGCCTTACTGAAGGTTTCTAGTTGTGACAAGAACACTGGTGATTATTAC Seq ID No. 49
TCTCCGTACTGGCGGAATGACTTCCAAAGATCAACACTGTTCTTGTGACCACTAATAATG

2401 GluAspSerTyrGluAspIleSerAlaTyrLeuLeuSerLysAsnAsnAlaIleGluPro
GAGGACAGTTATGAAGATATTTTCAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCA
CTCCTGTCAATACTTCTATAAAGTCGTATGAACGACTCATTTTTTGTACGGTAACTTGGT

<----- N-terminus of beta domain ----->

2461 ArgSerPheSerGlnAsnSerArgHisProSerThrArgGlnLysGlnPheAsnAlaThr
AGAAGCTTCTCCCAAGATTCTAGACACCCTAGCACTAGGCAAAAGCAATTTAATGCCACC
TCTTCGAAGAGGGTCTTAAGATCTGTGGGATCGTGATCCGTTTTTCGTTAAATTACGGTGG

2463 HIND3, 2475 ECORI, 2479 XBAI,

<-- IgA hinge ---><-- C-term. beta domain -->

2521 ProProThrProProThrProProValLeuLysArgHisGlnArgGluIleThrArgThr
CCTCCTACACCACCAACCCACCCAGTACTGAAACGCCATCAACGGGAAATAACTCGTACT
GGAGGATGTGGTGGTTGGGGTGGTCATGACTTTGCGGTAGTTGCCCTTTATTGAGCATGA

2544 SCAI,

2581 ThrLeuGlnSerAspGlnGluGluIleAspTyrAspAspThrIleSerValGluMetLys
ACTCTTCAGTCTGATCAAGAGGAAATTGACTATGATGATACCATATCAGTTGAAATGAAG
TGAGAAGTCAGACTAGTTCTCCTTTAACTGATACTACTATGGTATAGTCAACTTTACTTC

2592 BCLI,

Fig 38

Fig 39

ECOR1
NRU1
β region
α* 5 6 7 8 9 10

Seq ID No. 75 AsnSerArgHisProSer
F8-14E

Seq ID No. 77 2 AATTCGCGACACCCTAGC
F8-16E

Seq ID No. 79 GCGCTGTGGGATCGGTTTTGGGTGGTCAGAAC
F8-15E

Seq ID No. 76
11 12 13 14 15 16 17 18 19 20 21
GlnAsnProProValLeuLysArgHisGlnArgGluIleThr
F8-16E

Seq ID No. 78
21 22 23 24 25 26 27 28 29 30 31 32
TTTGCGGTAGTTGCCCTTTATTGC
F8-17E

Seq ID No. 81 ArgThrLeuGlnSerAsp
F8-14E

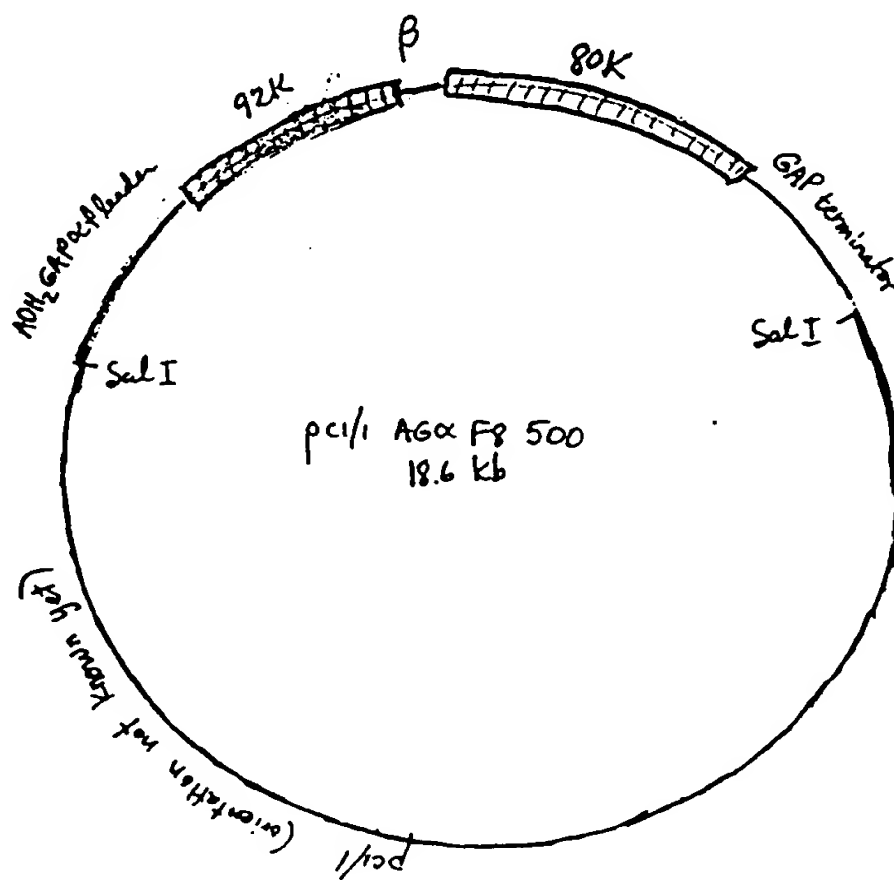
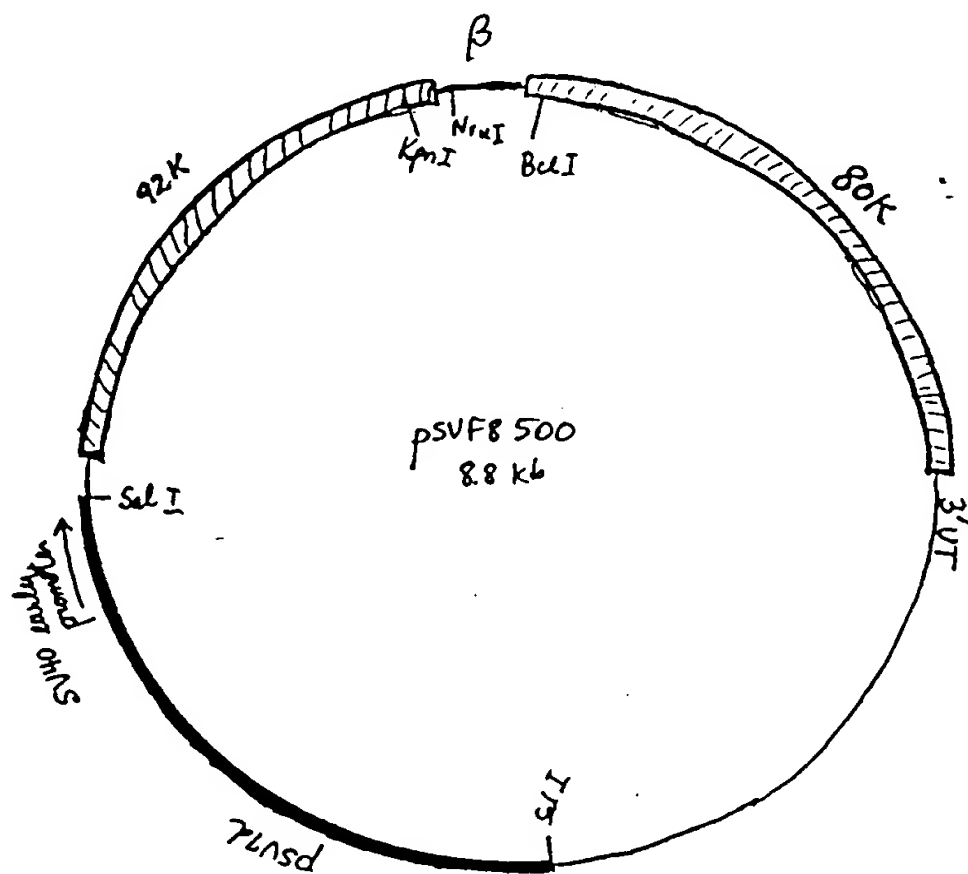
Seq ID No. 82 62 CGTACTCTTCAGTCT

Seq ID No. 83 GCATGAGAAGTCAGACTAG
F8-17E

1 ECOR1, 5 NRU1, 59 MLU1,
76 BCL1,

begin
80k
↓

Fig 40



Linkers for pSVF8-500B

end 92 19aa C terminal
to thrombin cleavage at 740

| | | |
|-----------|---|---------------|
| | SerArgHisProSerThrArgGlnLysGlnPheAspAlaThrProProValLeuLysArg | Seq ID No. 50 |
| | TCGCGACACCCTAGCACTAGGCAAAAGCAATTTAATGCCACCCCACCAGTCCTGAAACGC | Seq ID No. 51 |
| mutant | AGCGCTGTGGGATCGTGATCCGTTTTTCGTTAAATTACGGTGCGGTGGTCATGACTTTGCG | |
| wild type | (TT) (CT) | |
| | NRU1 | |

Start 80K
HisGlnArgGluIleThrArg
CATCAACGGGAAATAACGCGT
GTAGTTGCCCTTTATTGCGCA

MLU1
9aa N terminal to 80K

Fig 41